TEXT S1: SUPPORTING INFORMATION

DETAIL DESCRIPTION OF ESSENTIAL MODULES AND THEIR MOLECULAR BASIS

The core endogenous network of gastric epithelium is composed of eight core modules. References supporting the relations between the molecular-cellular endogenous agents in the network are listed in Supporting Table S1.

Cell cycle module

Cell cycle is a fundamental biological process of which is conserved in eukaryote. The gastric epithelium continuously renew through the life of animal due to proliferation of multipotent stem cells [1]. Cell cycle is divided into four phases: G_1, S, G_2, M. G_1-S phase was considered in this model, which is composed of cyclin D-Cdk4/6, cyclin E, Rb, E2F, p21 and p27[2]. Cyclin and cyclin-dependent kinase (CDK) constitute the core components of cell cycle process. Cyclin D-CDK4/6 complex initiates phosphorylation of Rb [2], which then dissociates from E2F resulting in activation of target genes transcription, like Cyclin E [3]. After the R point in late G1 phase, the Cyclin E-CDK2 complex to enable the phosphorylation of appropriate substrates required for entry into S phase. The level of Cyclin D was also regulated by transcription factors and extracellular signals, like c-Myc [4], β-catenin [5–7], NF-κB [8, 9], ERK [10], JNK/p38 [11], SHH [12]. On the other hand, the activities of Cyclin -CDK complexes were inhibited by CDK inhibitors, like p21 [13] and p27 [3, 14]. TGF-β elicited a number of downstream responses to antagonize cell proliferation, which can act throughout induce p21[15, 16]. The Myc could deregulate control of cell cycle progression through induce expression of Cyclin D, CDK4 and Cyclin E [4], and repressing expression of p21 [17, 18], p27 [19, 20]. Activation of p53 by DNA damage could induce cell cycle arrest, partially mediated by transcriptional activation of p21 [18, 21] and transcriptional inhibition of Myc [22, 23]. Gastric differentiation factors Sox2 exhibited cell cycle inhibition effect [24], while Shh exerted positive effects on cell cycle by induce expression of Cyclin D [12].

Cell death module

Cell death plays an essential role during the animal development and tissue homeostasis [25]. Apoptosis, an important form of programmed cell death, mediates physiological gastric epithelial cell loss in the normal gastric mucosa and chronic gastritis [26, 27]. Apoptosis is tightly controlled by either extracellular or intracellular signals. The center executor of apoptosis is caspases, of which activation is under dual control by both apoptosis activators and inhibitors such as Bcl-2, Bcl-XL, BAD, BAK-BAX, Bid and XIAP. The relatives of Bcl-2, such as Bad, Bax, Bak, and Bid, strive to pry open channels in the outer membrane of the mitochondria and thereby release cytochrome *c* into the surrounding cytosol [28, 29]. Yet Bcl-2 and Bcl-XL work oppositely to keep channels closed [30]. Once present in the cytosol, cytochrome *c* molecules associate with the Apaf-1 protein and form apoptosome and then proceeds to activate procaspase 9. The active caspase 9 then proceeds to activate procaspase 3, which executes apoptotic process [31–36]. Except the intrinsic apoptotic pathway, apoptosis can also be triggered through activated pro-apoptotic cell surface receptors, such as Fas and TNFR. These receptors act via the FAS-associated death domain (FADD) protein to assemble a death-inducing signaling complex (DISC), and the latter proceeds to activate caspases 8 and 10 [28, 37]. These then converge on the intrinsic apoptotic cascade by activating the caspases 3 [31–35], the latter cleaves and activates Bid [28], which initiates opening of the outer mitochondrial membrane channel, further activating the apoptotic cascade. Studies had revealed that a variety of stresses could cause a rapid increase in p53 levels. After p53 concentrations increase, the p53 bind to the promoters of a large of target genes and induce their transcription. Among the induced proteins are p21 [18, 21], Bax [38, 39], Fas [38, 39], Bcl-2 [38, 39] and IGF1-R [40, 41]. The survival signaling pathways through activation of the PI3kinase (PI3K)-Akt/PKB kinase pathway leads to Mdm2 phosphorylation and to the resulting p53 activation [42, 43]. The XIAPs bind to and inhibit caspases [44, 45]. XIAPs are bound and inhibited by a protein named SMAC/DIABLO, which is released from mitochondria along with cytochrome c during apoptosis [44]. In response to certain physiologic signals, NF-κB activates a large constituency of target genes involved in apoptosis; included among these are p53 [46], XIAP [46, 47], Bcl-2 [48] and Bcl-X_L [46, 47].

Inflammation

Cells are capable of sensing various deleterious conditions and respond by mounting a variety of stress responses. Normal signals like cytokines can induce inflammatory responses in cells [49]. Inflammation is a part of normal host protective attempt to eradicate injurious agents and to initiate the process of healing. However, inflammation also exerts influence on tumorigenesis [50]. Gastric cancer involves a transition from normal mucosa to gastritis, which eventually leads to adenocarcinoma [51]. *Helicobacter pylori*-induced gastritis is associated with increased risk of developing gastric adenocarcinoma. In this model, we focused on key inflammatory cytokines TNF-α, IL-1, IL-8, IL-10 and IFN-γ, which are associated with gastritis, atrophy response and development of gastric adenocarcinoma [52, 53]. IL-1 signaling activates the

c-Jun N-terminal kinase (JNK) and p38 MAPK pathway [54–56]. JNK phosphorylates proteins that are part of AP-1, in particularly c-Jun and ATF-2. It has been shown that JNK and c-Jun play a major role in IL-1-induced expression of genes encoding IL-8 [57–61], COX-2 [62–64] and IκB [65]. The JNK and p38 MAPK cascades [57–61] and NF-κB [46, 57, 65, 66] contribute to IL-8 gene expression. TNF signaling activates NF-κB through degradating IκB. NF-κB, a key transcriptional factor of inflammatory response and a critical bridge between inflammation and cancer, are also included [67]. Usually, NF-κB is sequestered in the cytoplasm by IκB (inhibitor of NF-κB). However, in response to diverse signals, IκB become phosphorylated and rapid degraded. As a result, NF-κB is liberated, and proceeds migrates into the nucleus and activates the expression of cohort of target genes, such as Bcl-2 [48], XIAP [46, 47], Myc [46], Cyclin D [8, 9] and COX-2 [46, 68, 69].

Angiogenesis

Angiogenesis is the physiological process beneficial for normal tissue growth and regeneration. However, it also represents a malignant transformation of tumor progression [70]. Under conditions of hypoxia, the HIF transcription factor accumulate, which then drives the expression of a number of genes whose products encourage angiogenesis. Prominent among these is VEGF [71]. VEGF/VEGFR could also be activated by IL-8 [72], IL-1 [73], HGF [74], Integrin [75] and PI3K/Akt signaling [76].

Metabolism

During cell growth and division, adjustment of energy metabolism is observed in neoplastic diseases. Cancer cells carry out increased aerobic glycolysis, a phenomenon known as the Warburg effect [77]. Some proteins, such as Myc, HIF, p53, AKT, Ras and β-catenin, are intimately linked to metabolic pathways through transcriptional or post-transcriptional regulation of metabolic enzymes [78].

Cell adhesion

Cell-to-cell interactions and their underlying extracellular matrix (ECM) present critical signals that regulate and maintain gastric epithelial differentiation, Those interaction mediator including E-cadherin and Integrins [79, 80]. In addition, cancer cells that participated in invasion and metastasis developed alterations in their attachment to other cells and to the extracellular matrix (ECM). The alteration best characterized by losing of E-cadherin, a key cell-to-cell adhesion molecule [81]. Those regulators include TGF-β[79] and a set of transcriptional factors like Zeb1/2 [82].

Gastric differentiation

The gastric epithelial associated factors that participate in gastric epithelium development and differentiation have been indentified as growth factors and transcription factors, such as Sox2, sonic hedgehog (Shh), Indian hedgehog (Ihh), gastrin, FGF10, Gata4, Gata6, BMP4, Runx3, Bapx1, Foxa1/2 and HoxA5. Recent data indicate that the most critical reprogramming factor, Cdx1/2, which inhibit expression of differentiated genes in gastric epithelium, is sufficient to direct the reprogramming of gastric epithelium cells into intestinal cells. On the other hand, the direct reprogramming factor of intestinal cells into gastric-liked epithelial cells has been demonstrated in several models, such as Sox2 and Shh. Therefore, the gastric cells state and intestinal cell state should be maintained by a set of master regulatory factors respectively.

Cdx2 is believed to be critical for maintaining intestinal epithelial cell phenotype [83, 84] and there have been several reports of it expression in intestinal metaplasia and intestinal type gastric carcinomas [85, 86]. Gastric expression of Cdx2 alone was sufficient to induce intestinal metaplasia in mice [87–89]. Beside, increased β-catenin expressions were significantly more frequent in intestinal-type gastric cancer compared with diffuse-type gastric carcinomas [90]. On the other hand, since, in adults, Sox2 expression is found in stomach and absent from the intestine [91]. Moreover, Sox2 participates in the development of foregut-derived organs, such as esophagus and stomach [92, 93], and are involved in regulation of stomach specific genes, pepsinogen and Muc5ac [94, 95]. Ectopic Sox2 expression is sufficient to redirect development fate of intestinal epithelium towards a premature gastric phenotype [96]. In addition, the loss of Sox2 expression and aberrant Cdx2 expression occur in intestinal metaplasia.

Growth factors

Various growth factors and hormones are expressed by mesenchymal cells but act on the epithelial compartment: for example, hepatocyte growth factor (HGF) is known to influence proliferation and differentiation of intestinal epithelial cells. The presence of EGF, HGF, IGF and KGF receptors in all glandular compartments clearly suggests the potential role of these growth factors either in the development or in the maintenance of specific gastric epithelial functions [3]. When the gastric mucosa is injured by inflammation or other insults, expression of growth factors and their receptors, such as EGF, IGF, EGFR family, and VEGFR

subtypes, are upregulated in epithelial or mesenchymal cells, and subsequently mucosal repair is promoted [97]. Ras can be activated by a number of signaling cascades radiating from growth factor receptors, such as EGF[98], HGF[99], VEGF [100] and Integrins [42, 43, 101, 102]. Ras activates Erk1 and Erk2 (MAPKs) via the Raf kinase [103]. The latter can then phosphorylate kinases in the cytoplasm that regulate transcription as well as transcription factors (Ets, Elk-1, SAP-1), which can then proceed to stimulate the expression of growth-regulating genes, such as Cyclin D [10], Myc [104], p21 [105] and HGF [106]. Ras protein is also capable to phosphorylate and activate phosphatidylinositol 3-kinase (PI3K) and AKT/PKB pathway. Once activated, Akt/PKB proceeds to phosphorylate and activate/inhibite a series of protein substrates, such as Bad [107], caspase-9 [108, 109], p21 [110] and GSK3β [111]. The PI3K-AKT pathway mainly aid cell survival and stimulate cell proliferation. The activation of PI3K and Akt/PKB is negatively control by PTEN [112].

DIFFERENTIAL EQUATIONS TO QUANTIFY THE WORKING ENDOGENOUS NETWORK

We translated the endogenous molecular network for gastric epithelium Figure 1 into mathematical format by employing sigmoidal functions. The quantitative descriptions are a set of coupled ordinary differential functions as follow. The meanings of parameters are in Methods. The computational codes are available upon request.

Supporting Table S1: Supporting information

The supporting information includes 3 parts: supporting methods, supporting tables and supporting figures.

$x(1) = Rb$	Unphosphorylated retinoblastoma protein
$x(2) = CyclinD/CDK4, 6$	Cyclin D/Cdk4,6 complex
$x(3) = CyclinE/CDK2$	Cyclin E/Cdk2 complex
$x(4) = c\text{-}Myc$	Myc/Max dimer
$x(5) = E2F$	E2F1,2 and E2F3a
$x(6) = p21$	
$x(7) = p27$	
$x(8) = p53$	
$x(9) = Caspase3, 7$	Caspase 3 and Caspase 7
$x(10) = Cytochrome c$	Mitochondrial proteins, including Cytochrome c, Apaf-1, Caspase 9, SMAC/ DIABLO, Endo G, AIF and CAD.
$x(11) = Caspase8, 10$	Caspase 8 and Caspase 10
$x(12) = XIAP$	
$x(13) = Bcl\text{-}2$	
$x(14) = Bcl\text{-}xL$	
$x(15) = Bid$	
$x(16) = BAD$	
$x(17) = Bax$	
$x(18) = Ras$	Ras super family, refers to HRAS, KRAS and NRAS.
$x(19) = Akt$	
$x(20) = PTEN$	
$x(21) = ERK$	The extracellular-signal-regulated kinase (ERK) pathway
$x(22) = JNK/p38$	The JUN N-terminal kinase (JNK) pathway and the p38 pathway
$x(23) = MKP$	Dual-specificity MAPK phosphatases; also known as dual specificity protein phosphatases (DUSPs), mainly refers to DUSP1 here.

$x(24) = VEGF/VEGFR$	VEGF and VEGF receptors
$x(25) = EGF/EGFR$	EGF family protein and ErbB family, mainly refers to EGF, HB-EGF, ErbB1/2.
$x(26) = IGF/EGFR$	Insulin-like growth factor (IGF) and IGF receptors
$x(27) = HGF/Met$	Hepatocyte growth factor(HGF) and c-Met receptor
$x(28) = Integrin/FAK$	Integrin/FAK signaling pathway
$x(29) = E\text{-}cadherin$	
$x(30) = Zeb1/2$	The ZEB family, including ZEB1 (also known as TCF8 and δEF1) and ZEB2 (also known as ZFXH1B and SMAD interacting protein 1 (SIP1))
$x(31) = \beta\text{-}catenin$	Wnt/β-catenin signaling pathway
$x(32) = HIF$	HIF family
$x(33) = NF\text{-}kB$	
$x(34) = ikB$	
$x(35) = TNF\text{-}\alpha$	
$x(36) = IL\text{-}10$	Interleukin-10 and its receptor
$x(37) = IL\text{-}1$	Interleukin-1 family, refers to IL-1α, IL-1β, and IL-18 and their receptors.
$x(38) = IL\text{-}8$	Interleukin-8 and receptors CXCR1 and CXCR2.
$x(39) = Fas$	Fas ligand or CD95L, and its receptors FasR and DcR3.
$x(40) = COX\text{-}2$	
$x(41) = TGF\text{-}\beta$	TGF-β family
$x(42) = IFN\text{-}\gamma$	
$x(43) = STAT3$	Signal transducer and activator of transcription 3
$x(44) = GSK\text{-}3\beta$	
$x(45) = Gastrin/CC2R$	Gastrin and it receptor
$x(46) = Sox2$	
$x(47) = Cdx2$	
$x(48) = Shh$	Sonic hedgehog signaling

$$\frac{dx(1)}{dt} = \frac{1}{1 + a(1) * x(2)^{n(1)} + a(2) * x(3)^{n(2)} + a(3) * x(9)^{n(3)}} - x(1);$$

$$\frac{dx(2)}{dt} = \frac{a(4) * x(4)^{n(4)} + a(5) * x(31)^{n(5)} + a(6) * x(33)^{n(6)} + a(7) * x(21)^{n(7)} + a(8) * x(22)^{n(8)} + a(9) * x(48)^{n(9)}}{1 + a(4) * x(4)^{n(4)} + a(5) * x(31)^{n(5)} + a(6) * x(33)^{n(6)} + a(7) * x(21)^{n(7)} + a(8) * x(22)^{n(8)} + a(9) * x(48)^{n(9)}} * \frac{1}{1 + a(10) * x(6)^{n(10)} + a(11) * x(44)^{n(11)} + a(12) * x(46)^{n(12)}} - x(2);$$

$$\frac{dx(3)}{dt} = \frac{a(13) * x(4)^{n(13)} + a(14) * x(5)^{n(14)}}{1 + a(13) * x(4)^{n(13)} + a(14) * x(5)^{n(14)}} * \frac{1}{1 + a(15) * x(6)^{n(15)} + a(16) * x(7)^{n(16)}} - x(3);$$

$$\frac{dx(4)}{dt} = \frac{a(17) * x(5)^{n(17)} + a(18) * x(19)^{n(18)} + a(19) * x(21)^{n(19)} + a(20) * x(22)^{n(20)} + a(21) * x(31)^{n(21)} + a(22) * x(33)^{n(22)} + a(23) * x(32)^{n(23)} + a(24) * x(48)^{n(24)}}{1 + a(17) * x(5)^{n(17)} + a(18) * x(19)^{n(18)} + a(19) * x(21)^{n(19)} + a(20) * x(22)^{n(20)} + a(21) * x(31)^{n(21)} + a(22) * x(33)^{n(22)} + a(23) * x(32)^{n(23)} + a(24) * x(48)^{n(24)}} * \frac{1}{1 + a(25) * x(8)^{n(25)} + a(26) * x(41)^{n(26)} + a(27) * x(42)^{n(27)} + a(28) * x(6)^{n(28)}} - x(4);$$

$$\frac{dx(5)}{dt} = \frac{a(29) * x(5)^{n(29)} + a(30) * x(4)^{n(30)}}{1 + a(29) * x(5)^{n(29)} + a(30) * x(4)^{n(30)}} * \frac{1}{1 + a(31) * x(1)^{n(31)} + a(32) * x(6)^{n(32)}} - x(5);$$

$$\frac{dx(6)}{dt} = \frac{a(33) * x(8)^{n(33)} + a(34) * x(41)^{n(34)} + a(35) * x(5)^{n(35)} + a(36) * x(42)^{n(36)} + a(37) * x(32)^{n(37)} + a(38) * x(21)^{n(38)} + a(39) * x(47)^{n(39)}}{1 + a(33) * x(8)^{n(33)} + a(34) * x(41)^{n(34)} + a(35) * x(5)^{n(35)} + a(36) * x(42)^{n(36)} + a(37) * x(32)^{n(37)} + a(38) * x(21)^{n(38)} + a(39) * x(47)^{n(39)}} * \frac{1}{1 + a(40) * x(4)^{n(40)} + a(41) * x(19)^{n(41)}} - x(6);$$

$$\frac{dx(7)}{dt} = \frac{a(42) * x(29)^{n(42)} + a(43) * x(41)^{n(43)} + a(44) * x(42)^{n(44)} + a(45) * x(20)^{n(45)} + a(46) * x(46)^{n(46)}}{1 + a(42) * x(29)^{n(42)} + a(43) * x(41)^{n(43)} + a(44) * x(42)^{n(44)} + a(45) * x(20)^{n(45)} + a(46) * x(46)^{n(46)}} * \frac{1}{1 + a(47) * x(4)^{n(47)} + a(48) * x(19)^{n(48)} + a(49) * x(3)^{n(49)} + a(50) * x(21)^{n(50)}} - x(7);$$

$$\frac{dx(8)}{dt} = \frac{a(51) * x(5)^{n(51)} + a(52) * x(4)^{n(52)} + a(53) * x(33)^{n(53)} + a(54) * x(10)^{n(54)}}{1 + a(51) * x(5)^{n(51)} + a(52) * x(4)^{n(52)} + a(53) * x(33)^{n(53)} + a(54) * x(10)^{n(54)}} * \frac{1}{1 + a(55) * x(19)^{n(55)}} - x(8);$$

$$\frac{dx(9)}{dt} = \frac{a(56) * x(10)^{n(56)} + a(57) * x(11)^{n(57)}}{1 + a(56) * x(10)^{n(56)} + a(57) * x(11)^{n(57)}} * \frac{1}{1 + a(58) * x(12)^{n(58)} + a(59) * x(6)^{n(59)}} - x(9);$$

$$\frac{dx(10)}{dt} = \frac{a(60) * x(16)^{n(60)} + a(61) * x(17)^{n(61)} + a(62) * x(15)^{n(62)} + a(63) * x(5)^{n(63)}}{1 + a(60) * x(16)^{n(60)} + a(61) * x(17)^{n(61)} + a(62) * x(15)^{n(62)} + a(63) * x(5)^{n(63)}} * \frac{1}{1 + a(64) * x(19)^{n(64)} + a(65) * x(12)^{n(65)}} - x(10);$$

$$\frac{dx(11)}{dt} = \frac{a(66) * x(39)^{n(66)} + a(67) * x(35)^{n(67)} + a(68) * x(37)^{n(68)}}{1 + a(66) * x(39)^{n(66)} + a(67) * x(35)^{n(67)} + a(68) * x(37)^{n(68)}} - x(11);$$

$$\frac{dx(12)}{dt} = \frac{a(69) * x(19)^{n(69)} + a(70) * x(33)^{n(70)}}{1 + a(69) * x(19)^{n(69)} + a(70) * x(33)^{n(70)}} * \frac{1}{1 + a(71) * x(10)^{n(71)}} - x(12);$$

$$\frac{dx(13)}{dt} = \frac{a(72) * x(24)^{n(72)} + a(73) * x(33)^{n(73)} + a(74) * x(21)^{n(74)} + a(75) * x(48)^{n(75)}}{1 + a(72) * x(24)^{n(72)} + a(73) * x(33)^{n(73)} + a(74) * x(21)^{n(74)} + a(75) * x(48)^{n(75)}} - x(13);$$

$$\frac{dx(14)}{dt} = \frac{a(80) * x(25)^{n(80)} + a(81) * x(26)^{n(81)} + a(82) * x(33)^{n(82)}}{1 + a(80) * x(25)^{n(80)} + a(81) * x(26)^{n(81)} + a(82) * x(33)^{n(82)}} - x(14);$$

$$\frac{dx(15)}{dt} = \frac{a(85) * x(11)^{n(85)}}{1 + a(85) * x(11)^{n(85)}} - x(15);$$

$$\frac{dx(16)}{dt} = \frac{a(86) * x(8)^{n(86)}}{1 + a(86) * x(8)^{n(86)}} * \frac{1}{1 + a(87) * x(19)^{n(87)} + a(88) * x(21)^{n(88)}} - x(16);$$

$$\frac{dx(17)}{dt} = \frac{a(89) * x(4)^{n(89)} + a(90) * x(8)^{n(90)}}{1 + a(89) * x(4)^{n(89)} + a(90) * x(8)^{n(90)}} * \frac{1}{1 + a(91) * x(13)^{n(91)} + a(92) * x(14)^{n(92)}} - x(17);$$

$$\frac{dx(18)}{dt} = \frac{a(93) * x(27)^{n(93)} + a(94) * x(25)^{n(94)} + a(95) * x(24)^{n(95)} + a(96) * x(28)^{n(96)}}{1 + a(93) * x(27)^{n(93)} + a(94) * x(25)^{n(94)} + a(95) * x(24)^{n(95)} + a(96) * x(28)^{n(96)}} - x(18);$$

$$\frac{dx(19)}{dt} = \frac{a(97) * x(38)^{n(97)} + a(98) * x(18)^{n(98)} + a(99) * x(26)^{n(99)} + a(100) * x(29)^{n(100)} + a(101) * x(28)^{n(101)} + a(102) * x(27)^{n(102)} + a(103) * x(24)^{n(103)} + a(104) * x(25)}{1 + a(97) * x(38)^{n(97)} + a(98) * x(18)^{n(98)} + a(99) * x(26)^{n(99)} + a(100) * x(29)^{n(100)} + a(101) * x(28)^{n(101)} + a(102) * x(27)^{n(102)} + a(103) * x(24)^{n(103)} + a(104) * x(2}$$

$$* \frac{1}{1 + a(106) * x(20)^{n(106)}} - x(19);$$

$$\frac{dx(20)}{dt} = \frac{1}{1 + a(107) * x(19)^{n(107)} + a(108) * x(33)^{n(108)} + a(109) * x(31)^{n(109)}} - x(20);$$

$$\frac{dx(21)}{dt} = \frac{a(110) * x(18)^{n(110)} + a(111) * x(28)^{n(111)} + a(112) * x(43)^{n(112)} + a(113) * x(45)^{n(113)}}{1 + a(110) * x(18)^{n(110)} + a(111) * x(28)^{n(111)} + a(112) * x(43)^{n(112)} + a(113) * x(45)^{n(113)}}$$

$$* \frac{1}{1 + a(114) * x(20)^{n(114)} + a(115) * x(23)^{n(115)}} - x(21);$$

$$\frac{dx(22)}{dt} = \frac{a(116) * x(41)^{n(116)} + a(117) * x(35)^{n(117)} + a(118) * x(37)^{n(118)} + a(119) * x(38)^{n(119)} + a(120) * x(24)^{n(120)} + a(121) * x(25)^{n(121)} + a(122) * x(45)^{n(122)}}{1 + a(116) * x(41)^{n(116)} + a(117) * x(35)^{n(117)} + a(118) * x(37)^{n(118)} + a(119) * x(38)^{n(119)} + a(120) * x(24)^{n(120)} + a(121) * x(25)^{n(121)} + a(122) * x(45)^{n(122)}}$$

$$* \frac{1}{1 + a(123) * x(20)^{n(123)} + a(124) * x(23)^{n(124)}} - x(22);$$

$$\frac{dx(23)}{dt} = \frac{a(125) * x(21)^{n(125)} + a(126) * x(22)^{n(126)}}{1 + a(125) * x(21)^{n(125)} + a(126) * x(22)^{n(126)}} - x(23);$$

$$\frac{dx(24)}{dt} = \frac{a(127) * x(38)^{n(127)} + a(128) * x(32)^{n(128)} + a(129) * x(19)^{n(129)} + a(130) * x(27)^{n(130)} + a(131) * x(40)^{n(131)} + a(132) * x(37)^{n(132)} + a(133) * x(28)^{n(133)} + a(134) *}{1 + a(127) * x(38)^{n(127)} + a(128) * x(32)^{n(128)} + a(12) * x(19)^{n(129)} + a(130) * x(27)^{n(130)} + a(131) * x(40)^{n(131)} + a(132) * x(37)^{n(132)} + a(133) * x(28)^{n(133)} + a(134)}$$

$$\frac{dx(25)}{dt} = \frac{a(135) * x(38)^{n(135)} + a(136) * x(28)^{n(136)}}{1 + a(135) * x(38)^{n(135)} + a(136) * x(28)^{n(136)}} - x(25);$$

$$\frac{dx(26)}{dt} = \frac{a(137) * x(32)^{n(137)}}{1 + a(137) * x(32)^{n(137)}} - x(26);$$

$$\frac{dx(27)}{dt} = \frac{a(139) * x(21)^{n(139)} + a(140) * x(32)^{n(140)} + a(141) * x(31)^{n(141)}}{1 + a(139) * x(21)^{n(139)} + a(140) * x(32)^{n(140)} + a(141) * x(31)^{n(141)}} - x(27);$$

$$\frac{dx(28)}{dt} = \frac{a(142) * x(25)^{n(142)} + a(143) * x(27)^{n(143)}}{1 + a(142) * x(25)^{n(142)} + a(143) * x(27)^{n(143)}} * \frac{1}{1 + a(144) * x(20)^{n(144)}} - x(28);$$

$$\frac{dx(29)}{dt} = \frac{1}{1 + a(145) * x(28)^{n}(145) + a(146) * x(37)^{n}(146) + a(147) * x(27)^{n}(147) + a(148) * x(30)^{n}(148) + a(149) * x(9)^{n}(149)} - x(29);$$

$$\frac{dx(30)}{dt} = \frac{a(150) * x(41)^{n(150)} + a(151) * x(33)^{n(151)}}{1 + a(150) * x(41)^{n(150)} + a(151) * x(33)^{n(151)}} * \frac{1}{1 + a(152) * x(8)^{n(152)}} - x(30);$$

$$\frac{dx(31)}{dt} = \frac{a(153)*x(45)^{n(153)} + a(154)*x(27)^{n(154)} + a(155)*x(25)^{n(155)} + a(156)*x(26)^{n(156)}}{1 + a(153)*x(45)^{n(153)} + a(154)*x(27)^{n(154)} + a(155)*x(25)^{n(155)} + a(156)*x(26)^{n(156)}} * \frac{1}{1 + a(157)*x(29)^{n(157)} + a(158)*x(44)^{n(158)} + a(159)*x(46)^{n(159)}} - x(31);$$

$$\frac{dx(32)}{dt} = \frac{a(160)*x(19)^{n(160)} + a(161)*x(33)^{n(161)} + a(162)*x(4)^{n(162)}}{1 + a(160)*x(19)^{n(160)} + a(161)*x(33)^{n(161)} + a(162)*x(4)^{n(162)}} * \frac{1}{1 + a(163)*x(8)^{n(163)}} - x(32);$$

$$\frac{dx(33)}{dt} = \frac{a(164)*x(22)^{n(164)}}{1 + a(164)*x(22)^{n(164)}} * \frac{1}{1 + a(165)*x(34)^{n(165)} + a(166)*x(8)^{n(166)}} - x(33);$$

$$\frac{dx(34)}{dt} = \frac{a(167)*x(33)^{n(167)} + a(168)*x(21)^{n(168)} + a(169)*x(22)^{n(169)}}{1 + a(167)*x(33)^{n(167)} + a(168)*x(21)^{n(168)} + a(169)*x(22)^{n(169)}} * \frac{1}{1 + a(170)*x(37)^{n(170)} + a(171)*x(19)^{n(171)} + a(172)*x(35)^{n(172)} + a(173)*x(39)^{n(173)} + a(174)*x(41)^{n(174)}} -$$

$$\frac{dx(35)}{dt} = \frac{a(175)*x(33)^{n(175)} + a(176)*x(21)^{n(176)} + a(177)*x(22)^{n(177)}}{1 + a(175)*x(33)^{n(175)} + a(176)*x(21)^{n(176)} + a(177)*x(22)^{n(177)}} * \frac{1}{1 + a(178)*x(36)^{n(178)}} - x(35);$$

$$\frac{dx(36)}{dt} = \frac{a(179)*x(35)^{n(179)} + a(180)*x(39)^{n(180)}}{1 + a(179)*x(35)^{n(179)} + a(180)*x(39)^{n(180)}} * \frac{1}{1 + a(181)*x(42)^{n(181)}} - x(36);$$

$$\frac{dx(37)}{dt} = \frac{a(182)*x(33)^{n(182)} + a(183)*x(22)^{n(183)}}{1 + a(182)*x(33)^{n(182)} + a(183)*x(22)^{n(183)}} * \frac{1}{1 + a(184)*x(37)^{n(184)}} - x(37);$$

$$\frac{dx(38)}{dt} = \frac{a(185)*x(33)^{n(185)} + a(186)*x(22)^{n(186)}}{1 + a(185)*x(33)^{n(185)} + a(186)*x(22)^{n(186)}} - x(38);$$

$$\frac{dx(39)}{dt} = \frac{a(187)*x(8)^{n(187)} + a(188)*x(33)^{n(188)} + a(189)*x(42)^{n(189)}}{1 + a(187)*x(8)^{n(187)} + a(188)*x(33)^{n(188)} + a(189)*x(42)^{n(189)}} * \frac{1}{1 + a(190)*x(18)^{n(189)}} - x(39);$$

$$\frac{dx(40)}{dt} = \frac{a(191)*x(33)^{n(191)} + a(192)*x(22)^{n(192)}}{1 + a(191)*x(33)^{n(191)} + a(192)*x(22)^{n(192)}} - x(40);$$

$$\frac{dx(41)}{dt} = \frac{a(193)*x(28)^{n(193)} + a(194)*x(32)^{n(194)}}{1 + a(193)*x(28)^{n(193)} + a(194)*x(32)^{n(194)}} * \frac{1}{1 + a(195)*x(33)^{n(195)}} - x(41);$$

$$\frac{dx(42)}{dt} = \frac{a(196)*x(37)^{n(196)}}{1 + a(196)*x(37)^{n(196)}} * \frac{1}{1 + a(197)*x(36)^{n(197)}} - x(42);$$

$$\frac{dx(43)}{dt} = \frac{a(198)*x(36)^{n(198)} + a(199)*x(45)^{n(199)} + a(200)*x(25)^{n(200)} + a(201)*x(27)^{n(201)}}{1 + a(198)*x(36)^{n(198)} + a(199)*x(45)^{n(199)} + a(200)*x(25)^{n(200)} + a(201)*x(27)^{n(201)}} * \frac{1}{1 + a(202)*x(41)^{n(2}$$

$$\frac{dx(44)}{dt} = \frac{1}{1 + a(203)*x(19)^{n(203)} + a(204)*x(33)^{n(204)}} - x(44);$$

$$\frac{dx(45)}{dt} = \frac{a(205)*x(31)^{n(205)}}{1 + a(205)*x(31)^{n(205)}} - x(45);$$

$$\frac{dx(46)}{dt} = \frac{a(206)*x(46)^{n(206)} + a(207)*x(48)^{n(207)} + a(208)*x(43)^{n(208)}}{1 + a(206)*x(46)^{n(206)} + a(207)*x(48)^{n(207)} + a(208)*x(43)^{n(208)}} * \frac{1}{1 + a(209)*x(42)^{n(209)}} - x(46);$$

$$\frac{dx(47)}{dt} = \frac{a(210)*x(31)^{n(210)} + a(211)*x(47)^{n(211)}}{1 + a(210)*x(31)^{n(210)} + a(211)*x(47)^{n(211)}} * \frac{1}{1 + a(212)*x(46)^{n(212)}} - x(47);$$

$$\frac{dx(48)}{dt} = \frac{a(213)*x(46)^{n(213)}}{1 + a(213)*x(46)^{n(213)}} * \frac{1}{1 + a(214)*x(47)^{n(214)} + a(215)*x(44)^{n(215)}} - x(48)$$

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SUPPLEMENTARY TABLES

Supplementary Table S1: Reference to each interaction in Figure 1

Components	Activation	References	Inhibition	References
Rb			Cyclin D/Cdk4,6*	[2]
			Cyclin E/Cdk2*	[2]
			Caspase 3§	[113]
Cyclin D/Cdk4,6	c-Myc‡	[4]	p21⁑	[13]
	β-catenin‡	[5–7]	GSK3β*	[114]
	NF-κB‡	[8, 9]	SOX2‡	[24]
	ERKǀ	[10]		
	JNK/p38ǀ	[11]		
	SHH‡	[12]		
Cyclin E/Cdk2	c-Myc‡	[4]	p21†	[14, 18]
	E2F‡	[3]	p27†	[3, 14]
c-Myc	E2F‡	[115]	p53‡	[22, 23]
	Akt|	[104]	TGF-β|	[116, 117]
	ERK|	[104]	IFN-γ|	[118–121]
	JNK/p38|	[104]	p21†	[105, 122]
	β-catenin‡	[123]		
	NF-κB‡	[46]		
	HIF2α‡	[121]		
	SHH‡	[12]		
E2F	E2F‡	[124]	Rb†	[125, 126]
	c-Myc‡	[127]	p21†	[128, 129]
p21	p53‡	[18, 21]	c-Myc‡	[17, 18]
	TGF-β‡	[15, 16]	Akt*	[110]
	E2F‡	[130, 131]		
	HIF‡	[132]		
	IFNγ|	[133–135]		
	ERK‡|	[105]		
	Cdx2‡	[91]		
p27	PTEN⁑	[136]	c-Myc‡	[19, 20]
	E-cadherin⁑	[137]	Akt|	[138]
	IFNγ|	[135, 139, 140]	Cyclin E/Cdk2*	[141]
	TGF-β|	[142]	ERK|	[143, 144]
	SOX2|	[24]		
p53	E2F‡	[145, 146]	Akt|	[42, 43]
	c-Myc‡	[20, 147, 148]		

(*Continued*)

Components	Activation	References	Inhibition	References
	NF-κB‡	[46]		
	Cytochrome *c* (Endo G, AIF, CAD)‖	[149]		
Caspase 3,7	Caspase 8,10§	[31–35]	p21†	[150, 151]
	Cytochrome *c*§	[31–36]	XIAP†	[44, 45]
Cytochrome *c*	Bad‖	[28]	Akt*	[108, 109]
	Bax‖	[28, 29]	XIAP†	[44, 45]
	Bid‖	[28]		
	E2F‡	[152, 153]		
Caspase 8,10	Fas†	[28]		
	TNF-α†	[28, 37]		
	IL-1†	[154]		
XIAP	Akt*	[155]	Cytochrome *c*†	[44]
	NF-κB‡	[46, 47]		
Bcl-2	VEGF※	[156]	p53‡	[38, 39]
	NF-κB‡	[48]	TGF-β‡‖	[157]
	ERK*	[158]	Bad†	[28]
	SHH‡	[12]	c-Myc‡	[159]
Bcl-x_L	EGF/EGFR‡‖	[160–163]	Bad†	[28]
	IGF/IGFR‡‖	[164, 165]	c-Myc‡	[159]
	NF-κB‡	[46, 47]		
Bid	Caspase 8,10§	[28]		
Bad	p53‡	[166]	Akt*	[107]
			ERK*	[167]
Bax/Bak	c-Myc‡	[159]	Bcl-2†	[168]
	p53‡	[38, 39]	Bcl-x_L†	[30]
Ras	HGF*‖	[99]		
	EGF*‖	[98]		
	VEGF*‖	[100]		
	Integrin*‖	[42, 43, 101, 102]		
PI3K-Akt	Ras*	[103]	PTEN*	[112]
	IL-8*‖	[72]		
	E-cadherin	[169]		
	Integrin*‖	[75, 170]		
	HGF*	[171, 172]		
	VEGF*	[100]		
	EGF*	[173]		

(*Continued*)

Components	Activation	References	Inhibition	References
	IGF*	[174–176]		
	TGF-β*	[157, 177]		
PTEN			Akt	[178, 179]
			NF-κB‡	[180]
			β-catenin‡|	[181]
ERK	Ras*	[103]	PTEN*	[112]
	Gastrin*|	[182]	MKP*	[183]
	Integrin*|	[101, 102]		
	STAT3※|	[184]		
JNK, p38	TGF-β*|	[185, 186]	PTEN*	[112]
	TNF-α*|	[187]	MKP*	[188, 189]
	IL-1*|	[54–56]		
	IL-8*|	[72]		
	EGF*|	[173]		
	VEGF*|	[100]		
	Gastrin*|	[182]		
MKP	ERK*	[190, 191]		
	JNK	[192]		
VEGF/VEGFR	IL-8*	[72]		
	HIF‡	[71]		
	Akt|	[76]		
	HGF/Met|	[74]		
	COX-2|	[193]		
	IL-1‡|	[73]		
	STAT3‡	[194]		
	Integrin*	[75]		
EGF/EGFR	IL-8*	[72]		
	Integrin*	[75]		
IGF-1R	HIF*	[195]	p53|	[40, 41]
HGF/SF c-Met	ERK‡|	[106]		
	HIF‡	[196]		
	β-catenin‡	[197, 198]		
Integrin-FAK	EGF*	[199–201]	PTEN*	[102]
	HGF*‡	[200, 202]		
E-cadherin			Integrin*	[203]
			IL-1β|	[204]
			Caspase 3,7§	[205]

(*Continued*)

Components	Activation	References	Inhibition	References
			c-Met*	[206–208]
			Zeb1/2‡	[209, 210]
ZEB1/2	TGF-β‡‖	[211, 212]	p53‖	[213, 214]
	NF-κB‡	[211, 212]		
β-catenin/LEF/TCF4 (cytoplasm)	Gastrin‡‖	[215]	E-cadherin†	[216]
			SOX2†	[217]
	HGF/c-Met*	[218]	GSK3β*	[219, 220]
	EGF*	[221]		
	IGF-1*	[222, 223]		
HIF	Akt*	[76, 224]	p53*	[225]
	NF-κB*	[226, 227]		
	c-Myc*			
NF-κB	JNK, p38‖	[228]	iκB†	[46, 229]
			STAT3‡	[230, 231]
iκB	NF-κB‡	[46, 232, 233]	TNF-α‖	[229]
	ERK‡‖	[65]	IL-1β‖	[65, 229, 234]
	JNK/p38‡‖	[65]	Akt*	[235–238]
			Fas‖	[239]
			TGF-β‖	[240]
TNF-α	NF-κB‡	[46]	IL-10‖	[241]
	ERK‡‖	[242]		
	JNK/p38‡‖	[242]		
IL-10	TNF-α‖	[243]	IFN-γ‖	[244]
	Fas※‖	[245, 246]		
IL-1	NF-κB‡		IL-1‖	[65, 247–250]
	JNK/p38‡‖	[65]		
IL-8	NF-κB‡	[46, 57, 65, 66]		
	JNK/p38‡‖	[57–61]		
Fas	p53‡	[38, 39]	Ras‖	[251]
	NF-κB‡	[46]		
	IFN-γ‡‖	[252]		
COX-2	NF-κB‡	[46, 68, 69]		
	JNK/p38‡	[62–64]		
TGF-β	Integrin†	[253, 254]	NF-κB‡‖	[240, 255]
	HIF‡	[256]		
IFN-γ	IL-1‖	[257–259]	IL-10‖	[260]

(*Continued*)

Components	Activation	References	Inhibition	References
STAT3	IL-10*	[184]	TGF-β*	[261, 262]
	Gastrin*	[182]		
	EGF*	[263, 264]		
	HGF*	[263]		
GSK3β			Akt*	[111]
			NF-κB[l]	[238]
Gastrin	β-catenin‡	[265, 266]		
SOX2	STAT3‡	[267]	IFN-γ[l]	[268]
	SHH‡	[269]		
	SOX2‡	[270]		
CDX2	β-catenin‡	[271]	SOX2‡	[272, 273]
	CDX2‡	[271]		
SHH	SOX2‡	[274]	CDX2‡	[275]
			GSK3β*	[12]

* The molecular mechanism of inhibition and activation interactions in the network.
* Components Phosphorylate or dephoephorylate targets, which result in their activation or inactivation;
§ Components cleave tagets, which result in their activation or inactivation;
‡ Components transcript target genes, and induce expression of targets;
† Components bind to targets, which inhibit or activate the activity of targets, or sequester them in the cytoplasm or nuclear;
[l] Components activate or inhibit targets indirectly, intermediates were abbreviated;
※ Components activate or inhibit targets through mechanisms still unknown.

Supplementary Table S2: Comparing model results and low throughput experimental data of the relative change of components

Components	Theoretical Results		Experimental Data	Experiment types
	P_1/A_1	P_2/A_1	GC/N	
Rb	↓	↓	↓[276]	RT-PCR
Cyclin D/Cdk4,6	↑	↑	↑[276, 277]	RT-PCR, IHC, WB
Cyclin E/Cdk2	↑	↑	↑[277]	RT-PCR, IHC, WB
E2F	↑	↑	↑[278]	RT-PCR, IHC, WB
Myc	↑	↑	↑[279, 280]	FISH, SB
p21	↑	↑	↓[281, 282]	IHC, PCR
p27	↓	↓	↓[277, 283]	RT-PCR, IHC, WB
p53	↑	↑	–[284, 285]	IHC
Caspase 3,7	↑	↑	↓[286, 287]	RT-PCR, IHC, WB
			↑[288, 289]	

(*Continued*)

Components	Theoretical Results		Experimental Data	Experiment types
	P_1/A_1	P_2/A_1	GC/N	
Cytochrome *c*	↑	↑	↓[290]	IHC
			↑[289]	
Caspase 8,10	↑	↑	↓[288]	IHC
			↑[289]	
XIAP	↑	↑	↑[291]	IHC
Bcl-2	↑	↑	↑[292]	IHC
Bcl-X_L	↑	↑	↑[293]	IHC
			↓[294]	IHC
Bid	↑	↑	N/A	
Bad	↑	↑	↑[295]	IHC
Bax	↑	↑	↑[294]	IHC
Ras	↑	↑	↑[296, 297]	IHC,
ERK	↑	↑	↑[298, 299]	WB, IHC
JNK, p38	↑	↑	↑[298, 299]	WB, IHC
MKP1/DUSP1	↑	↑	↑[300]	WB, RT-PCR
PTEN	↓	↓	↓[301]	RT-PCR
EGF/EGFR	↑	↑	↑[302–304]	IHC, SB
IGF/IGFR	↑	↑	↑[305, 306]	IHC
HGF/ c-Met	↑	↑	↑[279, 302]	IHC, SB, FISH
VEGF/VEGFR	↑	↑	↑[307, 308]	IHC
COX-2	↑	↑	↑[309–312]	IHC, WB
E-cadherin	↓	↓	↓[285, 313–316]	IHC, RT-PCR
ZEB1/2	↑	↑	↑[313]	RT-qPCR
β-catenin	↑	↑	↑[90, 317]	RT-PCR, IHC, WB
			↑[90, 318–320]	
GSK3β	↓	↓	↓[321]	IHC, WB
Integrin-FAK	↑	↑	↑[322, 323]	IHC, qRT-PCR, cDNA Microarrays
PI3K-Akt	↑	↑	↑[324]	RT-PCR, immunoblotting
HIF	↑	↑	↑[325–328]	IHC
NF-κB	↑	↑	↑[329, 330]	IHC
IκB	↑	↑	N/A	
TNF-α	↑	↑	↑[331, 332]	qRT-PCR
IL-10	↑	↑	↑[333–335]	RT-PCR
IL-1	↑	↑	↑[336, 337] [338]	RT-PCR
IL-8	↑	↑	↑[339, 340]	RT-PCR

(*Continued*)

Components	Theoretical Results		Experimental Data	Experiment types
	P_1/A_1	P_2/A_1	GC/N	
IFN-γ	↑	↑	N/A	
Fas	↑	↑	↑[341, 342]	WB, IHC
TGF-β	↑	↑	↑[334, 343, 344]	IHC
STAT3	↑	↑	↑[345, 346]	IHC
Gastrin	↑	↑	↑[85, 86]	IHC, RT-PCR
Sox2	↓	↓	↓[24]	qRT-PCR, WB
Cdx2	↑	↑	↑[347]	IHC
Shh	↑	↓	↑[348]	qRT-PCR, IHC
Consistency **(Theoretical/ Experimental)**	**97.5%(39/40)**	**95%(38/40)**		

If the ratios (for example, P_1 state to A_1 state) is greater than 1, we define the activity of the component is increased, otherwise is decreased. If the experimental results are conflict in independent studies, we define uncertain variation in component activity or expression of components between gastric cancer tissues and normal gastric epithelium. GC, gastric cancer;
N, normal gastric epithelium;
↑, means increased activity or expression of component;
↓, means decreased activity or expression of component;
__, non-significant or uncertain variation in component activity or expression;
N/A, means experimental results were not found. RT-PCR, reverse transcriptional polymerase chain reaction;
qRT-PCR, quantitative real-time polymerase chain reaction;
IHC, immunohistochemistry;
WB, western blot;
SB, southern blot;
FISH, fluorescence in situ hybridization;

Supplementary Table S3: Comparing model results and high-throughput experimental data of the relative change of components

	Theoretical Results		GSE19826	GSE22183	Gene Symbol
	P_1/A_1	P_2/A_1	GC/N	GC/N	
Rb	↓	↓	-	↓	RB1
Cyclin D/Cdk4,6	↑	↑	↑	↑	CCND1–3, CDK4, CDK6
Cyclin E/Cdk2	↑	↑	↑	↑	CCNE1–2, CDK2
Myc	↑	↑	↑	↑	MYC
E2F	↑	↑	↑	↑	E2F1, E2F2, E2F3
p21	↑	↑	-	↓	CDKN1A
p27	↓	↓	-	↑	CDKN1B
p53	↑	↑	-	↑	TP53

(*Continued*)

	Theoretical Results		GSE19826	GSE22183	Gene Symbol
	P_1/A_1	P_2/A_1	GC/N	GC/N	
Caspase 3,7	↑	↑	ND	↑	CASP3, CASP7
Cytochrome *c*	↑	↑	ND	↑	CYCS, CASP9, APAF1, DIABLO
Caspase 8,10	↑	↑	ND	↑	CASP8, CASP10
XIAP	↑	↑	↓	↑	XIAP
Bcl-2	↑	↑	↑	↑	BCL2
Bcl-xL	↑	↑	↑	↑	BCL2L1
Bid	↑	↑	↑	↑	BID
Bad	↑	↑	↓	-	BAD
Bax	↑	↑	↑	↑	BAX
Ras	↑	↑	↑	↑	KRAS, MRAS, RRAS, HRAS
Akt	↑	↑	↑	↑	AKT1, AKT2, AKT3
PTEN	↓	↓	-	↓	PTEN
ERK	↑	↑	↓	↑	MAPK1, MAPK3, MAPK6
JNK/p38	↑	↑	↑	↑	MAPK7–14
MKP	↑	↑	↑	↓	DUSP1
VEGF/VEGFR	↑	↑	-	↓	VEGFA
EGF/EGFR	↑	↑	↑	↑	EGF, EGFR, ERBB2
IGF/IGFR	↑	↑	↑	↓	IGF1, IGF1R, IGF2R
HGF/c-Met	↑	↑	↑	↑	HGF, MET
Integrin/FAK	↑	↑	↑	↑	ITGA2
E-cadherin	↓	↓	-	↑	CDH1
Zeb1/2	↑	↑	↑	↓	ZEB1, ZEB2
β-catenin	↑	↑	↑	↑	CTNNB1
HIF	↑	↑	↑	↓	HIF1A, ARNT, ARNT2, EPAS1
NFκB	↑	↑	↑	↑	NFKB1, NFKB2, RELA, RELB, REL
iκB	↑	↑	↑	↑	NFKBIA, NFKBIB, NFKBIE
TNF-α	↑	↑	↑	↑	TNF, TNFRSF1A, TNFRSF1B
IL10	↑	↑	↑	↑	IL10, IL10RA, IL10RB
IL1	↑	↑	ND	↑	IL1A, IL1B, IL1R1, IL1R2
IL8	↑	↑	↑	↑	IL8, CXCR1, CXCR2
Fas	↑	↑	↑	↑	FAS, FASLG
COX2	↑	↑	↓	↓	COX2
TGF-β	↑	↑	↑	ND	TGFB1, TGFB2, TGFB3, TGFBR1, TGFBR2, TGFBR3

(*Continued*)

	Theoretical Results		GSE19826	GSE22183	Gene Symbol
	P_1/A_1	P_2/A_1	GC/N	GC/N	
IFN-γ	↑	↑	↑	ND	IFNG, IFNGR1, IFNGR2
STAT3	↑	↑	↑	↓	STAT3
GSK3β	↓	↓	-	↓	GSK3B
Gastrin	↑	↑	↓	↑	GAST
Sox2	↓	↓	↓	↑	SOX2
Cdx2	↑	↑	↑	↑	CDX2
Shh	↑	↓	ND	ND	SHH, GLI1, GLI2, GLI3, PTCH1, PTCH2, SMO
GSE19826	**72.1%(40/47)**	**72.1%(40/47)**			
GSE22183	**73.3%(33/46)**	**71.1%(32/46)**			

If the ratios of one component between two stable states (for example, P1 state to A1 state) are greater than 1, we define the component activity as increased;
otherwise, the component activity is decreased.
GC, gastric cancer;
N, normal gastric epithelium;
↑, increased component activity or concentration;
↓, decreased component activity or concentration;
__, non-significant or uncertain variation in component activity or expression;
ND, non-determined variation in component expression.

Supplementary Table S4: Attractors of working endogenous network when $n = 3$, a = 7

Components	A_1	A_2	A_3	R_1	R_2	P_2	D
Rb	1.0000	1.0000	1.0000	0.9409	0.2155	0.1395	0.9586
Cyclin D/Cdk4,6	0.0006	0.0000	0.0000	0.1587	0.8000	0.8041	0.0010
Cyclin E/Cdk2	0.0000	0.0000	0.0000	0.1641	0.1963	0.7116	0.0000
Myc	0.0156	0.0098	0.0026	0.3064	0.3085	0.3072	0.0030
E2F	0.0000	0.0000	0.0000	0.0245	0.1843	0.6998	0.0000
p21	0.0000	0.0000	0.7298	0.1207	0.1220	0.1237	0.7872
p27	0.9340	0.9233	0.9233	0.1097	0.0828	0.0639	0.9297
p53	0.0000	0.0000	0.0000	0.0514	0.0524	0.1019	0.8154
Caspase 3,7	0.0000	0.0000	0.0000	0.0825	0.0821	0.0823	0.1844
Cytochrome c	0.0000	0.0000	0.0000	0.0346	0.0354	0.0633	0.8667
Caspase 8,10	0.0000	0.0000	0.0000	0.4939	0.4969	0.4960	0.1459
XIAP	0.0098	0.0098	0.0098	0.8654	0.8703	0.8688	0.0019
Bcl-2	0.0059	0.0000	0.0000	0.2846	0.2733	0.2707	0.0198
Bcl-xL	0.0000	0.0000	0.0000	0.7448	0.7439	0.7443	0.0000
Bid	0.0000	0.0000	0.0000	0.4576	0.4620	0.4606	0.0333
Bad	0.0000	0.0000	0.0000	0.0001	0.0001	0.0009	0.7831
Bax	0.0000	0.0000	0.0000	0.0415	0.0425	0.0432	0.7944
Ras	0.0000	0.0000	0.0000	0.9507	0.9546	0.9546	0.1580
Akt	0.1122	0.1122	0.1122	0.9537	0.9678	0.9678	0.1130
PTEN	0.9902	0.9902	0.9902	0.1337	0.0800	0.0796	0.9892
ERK	0.0000	0.0000	0.0000	0.4331	0.4388	0.4388	0.0495
JNK/p38	0.0000	0.0000	0.0000	0.4416	0.4432	0.4432	0.0203
MKP	0.0000	0.0000	0.0000	0.5395	0.5456	0.5456	0.0069
VEGF/VEGFR	0.0098	0.0098	0.0098	0.9560	0.9595	0.9593	0.0718
EGF/EGFR	0.0000	0.0000	0.0000	0.8483	0.8574	0.8572	0.0000
IGF/IGFR	0.0000	0.0000	0.0000	0.8201	0.8224	0.8143	0.0000
HGF/c-Met	0.0000	0.0000	0.0000	0.8384	0.9093	0.9091	0.0050
Integrin/FAK	0.0000	0.0000	0.0000	0.8789	0.9031	0.9031	0.0000
E-cadherin	1.0000	1.0000	1.0000	0.0790	0.0704	0.0706	0.9586
Zeb1/2	0.0000	0.0000	0.0000	0.7033	0.7035	0.7006	0.0000
β-catenin	0.0000	0.0000	0.0000	0.1746	0.8805	0.8843	0.0000
HIF	0.0098	0.0098	0.0098	0.8683	0.8730	0.8673	0.0022
NFκB	0.0000	0.0000	0.0000	0.3751	0.3776	0.3753	0.0004
iκB	0.0000	0.0000	0.0000	0.0603	0.0592	0.0590	0.0060
TNF-α	0.0000	0.0000	0.0000	0.4483	0.4501	0.4497	0.0066
IL10	0.0000	0.0000	0.0000	0.3694	0.3718	0.3714	0.1459

(*Continued*)

Components	A_1	A_2	A_3	R_1	R_2	P_2	D
IL1	0.0000	0.0000	0.0000	0.3666	0.3681	0.3673	0.0020
IL8	0.0000	0.0000	0.0000	0.4930	0.4965	0.4948	0.0020
Fas	0.0000	0.0000	0.0000	0.0420	0.0422	0.0421	0.4961
COX2	0.0000	0.0000	0.0000	0.4930	0.4965	0.4948	0.0020
TGF-β	0.0000	0.0000	0.0000	0.6595	0.6590	0.6619	0.0000
IFN-γ	0.0000	0.0000	0.0000	0.1895	0.1903	0.1896	0.0000
STAT3	0.0000	0.0000	0.0000	0.2983	0.3107	0.3081	0.0333
GSK3β	0.9902	0.9902	0.9902	0.1344	0.1295	0.1296	0.9892
Gastrin	0.0000	0.0000	0.0000	0.0359	0.8270	0.8288	0.0000
Sox2	0.7389	0.0000	0.0000	0.8485	0.2009	0.1949	0.8048
Cdx2	0.0000	0.0000	0.7370	0.0068	0.8528	0.8581	0.0000
Shh	0.0947	0.0000	0.0000	0.7969	0.0100	0.0091	0.1031

A (A_1, A_2 and A_3), R (R_1 and R_2), P (P_1 and P_2) are point attractors, D is a cyclic attractor. Dynamical trajectories of Caspase 8/10, Bid, Fas, VEGF/VEGFR, IL10, Ras and STAT3 is showed in Supplemnetary Figure S1.

Supplementary Table S5: Attractors of working endogenous network when $n = 3$, a = 8

Components	A_1	A_2	A_3	R_1	R_2	P_2	D
Rb	1.0000	1.0000	1.0000	0.9443	0.1867	0.1063	0.9698
Cyclin D/Cdk4,6	0.0005	0.0000	0.0000	0.1432	0.8126	0.8186	0.0006
Cyclin E/Cdk2	0.0000	0.0000	0.0000	0.1581	0.1961	0.7949	0.0000
Myc	0.0142	0.0082	0.0016	0.2883	0.2903	0.2890	0.0020
E2F	0.0000	0.0000	0.0000	0.0208	0.1872	0.7883	0.0000
p21	0.0000	0.0000	0.8024	0.1073	0.1087	0.1104	0.8219
p27	0.9447	0.9328	0.9328	0.0986	0.0760	0.0534	0.9404
p53	0.0000	0.0000	0.0000	0.0462	0.0477	0.0978	0.8441
Caspase 3,7	0.0000	0.0000	0.0000	0.0785	0.0783	0.0784	0.1562
Cytochrome c	0.0000	0.0000	0.0000	0.0379	0.0382	0.0599	0.8921
Caspase 8,10	0.0000	0.0000	0.0000	0.5073	0.5095	0.5085	0.2012
XIAP	0.0082	0.0082	0.0082	0.8825	0.8858	0.8846	0.0013
Bcl-2	0.0062	0.0000	0.0000	0.2713	0.2616	0.2587	0.0117
Bcl-xL	0.0000	0.0000	0.0000	0.7667	0.7649	0.7656	0.0000
Bid	0.0000	0.0000	0.0000	0.5109	0.5142	0.5127	0.0197
Bad	0.0000	0.0000	0.0000	0.0001	0.0001	0.0008	0.8188
Bax	0.0000	0.0000	0.0000	0.0339	0.0348	0.0353	0.8285
Ras	0.0000	0.0000	0.0000	0.9590	0.9617	0.9617	0.1121
Akt	0.1009	0.1009	0.1009	0.9625	0.9732	0.9732	0.1014
PTEN	0.9918	0.9918	0.9918	0.1167	0.0695	0.0690	0.9911
ERK	0.0000	0.0000	0.0000	0.4134	0.4176	0.4177	0.0353
JNK/p38	0.0000	0.0000	0.0000	0.4198	0.4210	0.4210	0.0128
MKP	0.0000	0.0000	0.0000	0.5364	0.5412	0.5413	0.0049
VEGF/VEGFR	0.0082	0.0082	0.0082	0.9632	0.9656	0.9654	0.0480
EGF/EGFR	0.0000	0.0000	0.0000	0.8726	0.8784	0.8782	0.0000
IGF/IGFR	0.0000	0.0000	0.0000	0.8465	0.8478	0.8396	0.0000
HGF/c-Met	0.0000	0.0000	0.0000	0.8599	0.9218	0.9218	0.0037
Integrin/FAK	0.0000	0.0000	0.0000	0.9009	0.9187	0.9187	0.0000
E-cadherin	1.0000	1.0000	1.0000	0.0651	0.0592	0.0593	0.9698
Zeb1/2	0.0000	0.0000	0.0000	0.7240	0.7236	0.7207	0.0000
β-catenin	0.0000	0.0000	0.0000	0.1561	0.8884	0.8939	0.0000
HIF	0.0082	0.0082	0.0082	0.8848	0.8879	0.8820	0.0015
NFκB	0.0000	0.0000	0.0000	0.3711	0.3730	0.3706	0.0002
iκB	0.0000	0.0000	0.0000	0.0536	0.0529	0.0527	0.0043
TNF-α	0.0000	0.0000	0.0000	0.4328	0.4341	0.4337	0.0048
IL10	0.0000	0.0000	0.0000	0.3714	0.3732	0.3728	0.2012

(*Continued*)

Components	A_1	A_2	A_3	R_1	R_2	P_2	D
IL1	0.0000	0.0000	0.0000	0.3623	0.3635	0.3627	0.0013
IL8	0.0000	0.0000	0.0000	0.5002	0.5030	0.5011	0.0013
Fas	0.0000	0.0000	0.0000	0.0397	0.0398	0.0396	0.5761
COX2	0.0000	0.0000	0.0000	0.5002	0.5030	0.5011	0.0013
TGF-β	0.0000	0.0000	0.0000	0.6525	0.6514	0.6546	0.0000
IFN-γ	0.0000	0.0000	0.0000	0.1955	0.1960	0.1953	0.0000
STAT3	0.0000	0.0000	0.0000	0.2841	0.2941	0.2912	0.0197
GSK3β	0.9918	0.9918	0.9918	0.1171	0.1138	0.1139	0.9911
Gastrin	0.0000	0.0000	0.0000	0.0295	0.8487	0.8510	0.0000
Sox2	0.8095	0.0000	0.0000	0.8549	0.1979	0.1904	0.8326
Cdx2	0.0000	0.0000	0.8090	0.0049	0.8612	0.8684	0.0000
Shh	0.0919	0.0000	0.0000	0.8227	0.0095	0.0084	0.0946

A (A_1, A_2 and A_3), R (R_1 and R_2), P (P_1 and P_2) are point attractors, D is a cyclic attractor. Dynamical trajectories of Caspase 8/10, Bid, Fas, VEGF/VEGFR, IL10, Ras and STAT3 is showed in Supplementary Figure S1.

Supplementary Table S6: Attractors of working endogenous network when *n* = 3, a = 10

Components	A_1	A_2	A_3	R_1	R_2	P_1	P_2	D
Rb	1.0000	1.0000	1.0000	0.9473	0.1495	0.1425	0.0763	0.9835
Cyclin D/ Cdk4,6	0.0003	0.0000	0.0000	0.1224	0.8241	0.1221	0.8328	0.0003
Cyclin E/ Cdk2	0.0000	0.0000	0.0000	0.1501	0.2075	0.8432	0.8586	0.0001
Myc	0.0107	0.0056	0.0008	0.2617	0.2635	0.2605	0.2625	0.0010
E2F	0.0000	0.0000	0.0000	0.0160	0.2018	0.8211	0.8556	0.0512
p21	0.0000	0.0000	0.8621	0.0889	0.0894	0.0916	0.0907	0.8684
p27	0.9582	0.9470	0.9470	0.0828	0.0651	0.0535	0.0420	0.9560
p53	0.0000	0.0000	0.0000	0.0392	0.0411	0.0852	0.0840	0.8836
Caspase 3,7	0.0000	0.0000	0.0000	0.0707	0.0704	0.0707	0.0704	0.1189
Cytochrome c	0.0000	0.0000	0.0000	0.0387	0.0385	0.0505	0.0500	0.9278
Caspase 8,10	0.0000	0.0000	0.0000	0.5274	0.5291	0.5264	0.5282	0.4243
XIAP	0.0056	0.0056	0.0056	0.9049	0.9075	0.9042	0.9069	0.0006
Bcl-2	0.0051	0.0000	0.0000	0.2508	0.2434	0.2481	0.2409	0.0332
Bcl-xL	0.0000	0.0000	0.0000	0.7939	0.7918	0.7949	0.7925	0.0000
Bid	0.0000	0.0000	0.0000	0.5947	0.5969	0.5933	0.5957	0.4331
Bad	0.0000	0.0000	0.0000	0.0001	0.0001	0.0006	0.0005	0.8665
Bax	0.0000	0.0000	0.0000	0.0247	0.0254	0.0251	0.0257	0.8731
Ras	0.0000	0.0000	0.0000	0.9692	0.9707	0.9691	0.9707	0.4767
Akt	0.0826	0.0826	0.0826	0.9691	0.9795	0.9690	0.9795	0.0836

(*Continued*)

Components	A_1	A_2	A_3	R_1	R_2	P_1	P_2	D
PTEN	1.0000	1.0000	1.0000	0.1066	0.0594	0.1068	0.0588	1.0000
ERK	0.0000	0.0000	0.0000	0.3803	0.3833	0.3803	0.3833	0.0595
JNK/p38	0.0000	0.0000	0.0000	0.3846	0.3855	0.3846	0.3855	0.0433
MKP	0.0000	0.0000	0.0000	0.5281	0.5318	0.5281	0.5318	0.0029
VEGF/ VEGFR	0.0056	0.0056	0.0056	0.9720	0.9735	0.9719	0.9734	0.4500
EGF/EGFR	0.0000	0.0000	0.0000	0.9021	0.9057	0.9019	0.9056	0.0000
IGF/IGFR	0.0000	0.0000	0.0000	0.8811	0.8819	0.8744	0.8756	0.0000
HGF/c-Met	0.0000	0.0000	0.0000	0.8892	0.9381	0.8876	0.9384	0.0021
Integrin/FAK	0.0000	0.0000	0.0000	0.9237	0.9381	0.9235	0.9382	0.0000
E-cadherin	1.0000	1.0000	1.0000	0.0485	0.0450	0.0487	0.0451	0.9835
Zeb1/2	0.0000	0.0000	0.0000	0.7529	0.7521	0.7505	0.7498	0.0000
β-catenin	0.0000	0.0000	0.0000	0.1315	0.8916	0.1312	0.8995	0.0000
HIF	0.0056	0.0056	0.0056	0.9065	0.9090	0.9013	0.9041	0.0007
NFκB	0.0000	0.0000	0.0000	0.3621	0.3636	0.3601	0.3617	0.0001
iκB	0.0000	0.0000	0.0000	0.0445	0.0439	0.0444	0.0437	0.0017
TNF-α	0.0000	0.0000	0.0000	0.4066	0.4075	0.4063	0.4071	0.0017
IL10	0.0000	0.0000	0.0000	0.3711	0.3723	0.3707	0.3720	0.4243
IL1	0.0000	0.0000	0.0000	0.3539	0.3547	0.3532	0.3541	0.0008
IL8	0.0000	0.0000	0.0000	0.5107	0.5130	0.5088	0.5113	0.0008
Fas	0.0000	0.0000	0.0000	0.0355	0.0356	0.0354	0.0355	0.4193
COX2	0.0000	0.0000	0.0000	0.5107	0.5130	0.5088	0.5113	0.0008
TGF-β	0.0000	0.0000	0.0000	0.6366	0.6350	0.6396	0.6379	0.0000
IFN-γ	0.0000	0.0000	0.0000	0.2032	0.2035	0.2026	0.2030	0.0000
STAT3	0.0000	0.0000	0.0000	0.2618	0.2691	0.2590	0.2665	0.4331
GSK3β	0.9944	0.9944	0.9944	0.0945	0.0919	0.0946	0.0920	0.9942
Gastrin	0.0000	0.0000	0.0000	0.0222	0.8764	0.0221	0.8792	0.0000
Sox2	0.8671	0.0000	0.0000	0.8551	0.1964	0.8558	0.1878	0.8860
Cdx2	0.0000	0.0000	0.8670	0.0031	0.8658	0.0030	0.8753	0.0000
Shh	0.0800	0.0000	0.0000	0.8549	0.0094	0.8552	0.0081	0.0808

A (A_1, A_2 and A_3), R (R_1 and R_2), P (P_1 and P_2) are point attractors, D is a cyclic attractor. Dynamical trajectories of Caspase 8/10, Bid, Fas, VEGF/VEGFR, IL10, Ras and STAT3 is showed in Supplementary Figure S1.

Supplementary Table S7: Attractors of working endogenous network when $n = 4$, $a = 16$

Components	A_1	A_2	A_3	R_1	R_2	P_1	P_2	D
Rb	1.0000	1.0000	1.0000	0.9997	0.0737	0.0805	0.0400	0.9995
Cyclin D/ Cdk4,6	0.0000	0.0000	(0.0000)	0.0659	0.9414	0.0659	0.9414	0.0000
Cyclin E/ Cdk2	0.0000	0.0000	0.0000	0.0093	0.0094	0.9192	0.9194	0.0000
Myc	0.0003	0.0002	0.0000	0.1556	0.1561	0.1563	0.1568	0.0000
E2F	0.0000	0.0000	0.0000	0.0005	0.0094	0.9186	0.9194	0.0000
p21	0.0000	0.0000	0.9195	0.0583	0.0595	0.0595	0.0600	0.9233
p27	0.9773	0.9695	0.9695	0.0564	0.0499	0.0336	0.0297	0.9775
p53	0.0000	0.0000	0.0000	0.0135	0.0135	0.0567	0.0566	0.9312
Caspase 3,7	0.0000	0.0000	0.0000	0.0321	0.0322	0.0321	0.0322	0.0737
Cytochrome c	0.0000	(0.0000)	(0.0000)	0.0125	0.0126	0.0321	0.0321	0.9588
Caspase 8,10	0.0000	0.0000	(0.0000)	0.4672	0.4680	0.4672	0.4679	0.4761
XIAP	0.0002	0.0002	0.0002	0.9395	0.9396	0.9395	0.9396	0.0000
Bcl-2	0.0001	0.0000	0.0000	0.1538	0.1502	0.1538	0.1501	0.0019
Bcl-xL	0.0000	0.0000	(0.0000)	0.9514	0.9514	0.9513	0.9512	0.0000
Bid	0.0000	0.0000	0.0000	0.4325	0.4342	0.4325	0.4341	0.0152
Bad	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.9232
Bax	0.0000	0.0000	0.0000	0.0007	0.0007	0.0007	0.0007	0.9234
Ras	0.0000	0.0000	0.0000	0.9813	0.9821	0.9813	0.9821	0.0464
Akt	0.0554	0.0554	0.0554	0.9882	0.9887	0.9882	0.9887	0.0555
PTEN	0.9998	0.9998	0.9998	0.0605	0.0319	0.0605	0.0319	0.9998
ERK	(0.0000)	(0.0000)	(0.0000)	0.4311	0.4324	0.4311	0.4324	0.0082
JNK/p38	0.0000	0.0000	0.0000	0.4335	0.4336	0.4335	0.4336	0.0027
MKP	0.0000	(0.0000)	(0.0000)	0.5277	0.5295	0.5277	0.5295	0.0000
VEGF/ VEGFR	0.0002	0.0002	0.0002	0.9821	0.9828	0.9821	0.9828	0.0157
EGF/EGFR	(0.0000)	(0.0000)	0.0000	0.9345	0.9353	0.9345	0.9353	0.0000
IGF/IGFR	0.0000	0.0000	0.0000	0.9257	0.9258	0.9255	0.9256	0.0000
HGF/c-Met	0.0000	0.0000	0.0000	0.9287	0.9653	0.9286	0.9653	0.0000
Integrin/FAK	0.0000	0.0000	(0.0000)	0.9600	0.9631	0.9600	0.9631	0.0000
E-cadherin	1.0000	1.0000	1.0000	0.0286	0.0269	0.0286	0.0269	0.9995
Zeb1/2	0.0000	0.0000	(0.0000)	0.8470	0.8467	0.8469	0.8466	0.0000
β-catenin	0.0000	0.0000	(0.0000)	0.0689	0.9803	0.0689	0.9802	0.0000
HIF	0.0002	0.0002	0.0002	0.9395	0.9396	0.9394	0.9395	0.0000
NFκB	0.0000	(0.0000)	(0.0000)	0.3609	0.3613	0.3609	0.3612	0.0000
iκB	0.0000	(0.0000)	(0.0000)	0.0260	0.0260	0.0260	0.0260	0.0000

(*Continued*)

Components	A_1	A_2	A_3	R_1	R_2	P_1	P_2	D
TNF-α	0.0000	(0.0000)	(0.0000)	0.4418	0.4422	0.4418	0.4422	0.0000
IL10	0.0000	0.0000	(0.0000)	0.3748	0.3756	0.3748	0.3756	0.4761
IL1	0.0000	(0.0000)	(0.0000)	0.3594	0.3597	0.3594	0.3597	0.0000
IL8	0.0000	(0.0000)	(0.0000)	0.4555	0.4560	0.4554	0.4560	0.0000
Fas	0.0000	0.0000	(0.0000)	0.0139	0.0139	0.0139	0.0139	0.7964
COX2	0.0000	(0.0000)	(0.0000)	0.4555	0.4560	0.4554	0.4560	0.0000
TGF-β	0.0000	0.0000	0.0000	0.7574	0.7569	0.7575	0.7570	0.0000
IFN-γ	(0.0000)	(0.0000)	(0.0000)	0.1602	0.1602	0.1602	0.1602	0.0000
STAT3	0.0000	0.0000	0.0000	0.1534	0.1559	0.1533	0.1559	0.0152
GSK3β	0.9998	0.9998	0.9998	0.0605	0.0604	0.0605	0.0604	0.9998
Gastrin	(0.0000)	(0.0000)	0.0000	0.0004	0.9366	0.0004	0.9366	0.0000
Sox2	0.9196	(0.0000)	(0.0000)	0.9516	0.0093	0.9516	0.0093	0.9220
Cdx2	(0.0000)	(0.0000)	0.9196	0.0000	0.9664	0.0000	0.9664	0.0000
Shh	0.0541	0.0000	(0.0000)	0.9290	0.0000	0.9290	0.0000	0.0543

A (A_1, A_2 and A_3), R (R_1 and R_2), P (P_1 and P_2) are point attractors, D is a cyclic attractor. Dynamical trajectories of Caspase 8/10, Bid, Fas, VEGF/VEGFR, IL10, Ras and STAT3 is showed in Supplementary Figure S1.

Supplementary Table S8: Attractors of working endogenous network when $n = 5$, a = 32

Components	A_1	A_2	A_3	R_1	R_2	P_1	P_2	D
Rb	1.0000	1.0000	1.0000	1.0000	0.0352	0.0362	0.0182	1.0000
Cyclin D/ Cdk4,6	0.0000	(0.0000)	0.0000	0.0320	0.9696	0.0320	0.9696	0.0000
Cyclin E/ Cdk2	0.0000	(0.0000)	0.0000	0.0001	0.0001	0.9638	0.9638	0.0000
Myc	0.0000	0.0000	0.0000	0.0707	0.0706	0.0709	0.0708	0.0000
E2F	0.0000	(0.0000)	0.0000	0.0000	0.0001	0.9638	0.9638	0.0000
p21	0.0000	(0.0000)	0.9638	0.0304	0.0307	0.0307	0.0308	0.9990
p27	0.9891	0.9846	0.9846	0.0299	0.0284	0.0165	0.0157	0.9997
p53	0.0000	(0.0000)	0.0000	0.0047	0.0047	0.0300	0.0300	0.9990
Caspase 3,7	0.0000	(0.0000)	0.0000	0.0121	0.0121	0.0121	0.0121	0.0010
Cytochrome c	0.0000	(0.0000)	0.0000	0.0022	0.0022	0.0162	0.0162	0.9997
Caspase 8,10	0.0000	(0.0000)	0.0000	0.4387	0.4389	0.4387	0.4389	0.2113
XIAP	0.0000	0.0000	0.0000	0.9691	0.9691	0.9691	0.9691	0.0000
Bcl-2	0.0000	(0.0000)	(0.0000)	0.0703	0.0692	0.0703	0.0692	0.0005
Bcl-xL	0.0000	(0.0000)	0.0000	0.9818	0.9818	0.9818	0.9818	0.0000
Bid	0.0000	(0.0000)	0.0000	0.3422	0.3426	0.3422	0.3426	0.5745
Bad	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.9990
Bax	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000	0.0000	0.9990

(*Continued*)

Components	A_1	A_2	A_3	R_1	R_2	P_1	P_2	D
Ras	0.0000	(0.0000)	0.0000	0.9913	0.9915	0.9913	0.9915	0.9754
Akt	0.0294	0.0294	0.0294	0.9946	0.9947	0.9946	0.9947	0.0010
PTEN	1.0000	1.0000	1.0000	0.0309	0.0159	0.0309	0.0159	1.0000
ERK	0.0000	0.0000	0.0000	0.4420	0.4425	0.4420	0.4425	0.0010
JNK/p38	0.0000	(0.0000)	0.0000	0.4432	0.4431	0.4432	0.4431	0.0010
MKP	0.0000	(0.0000)	0.0000	0.5208	0.5215	0.5208	0.5215	0.0000
VEGF/ VEGFR	0.0000	0.0000	0.0000	0.9914	0.9916	0.9914	0.9916	0.9911
EGF/EGFR	0.0000	0.0000	0.0000	0.9673	0.9675	0.9673	0.9675	0.0000
IGF/IGFR	0.0000	0.0000	0.0000	0.9647	0.9647	0.9647	0.9647	0.0000
HGF/c-Met	0.0000	0.0000	0.0000	0.9654	0.9832	0.9654	0.9832	0.0000
Integrin/FAK	0.0000	(0.0000)	(0.0000)	0.9818	0.9826	0.9818	0.9826	0.0000
E-cadherin	1.0000	1.0000	1.0000	0.0126	0.0122	0.0126	0.0122	1.0000
Zeb1/2	0.0000	(0.0000)	0.0000	0.9294	0.9295	0.9294	0.9295	0.0000
β-catenin	0.0000	(0.0000)	(0.0000)	0.0328	0.9910	0.0328	0.9910	0.0000
HIF	0.0000	0.0000	0.0000	0.9691	0.9691	0.9691	0.9691	0.0000
NFκB	0.0000	(0.0000)	0.0000	0.3536	0.3535	0.3536	0.3535	0.0000
iκB	0.0000	0.0000	0.0000	0.0122	0.0122	0.0122	0.0122	0.0000
TNF-α	0.0000	0.0000	0.0000	0.4515	0.4516	0.4515	0.4516	0.0000
IL10	0.0000	(0.0000)	0.0000	0.3747	0.3750	0.3747	0.3750	0.2113
IL1	0.0000	0.0000	0.0000	0.3554	0.3553	0.3554	0.3553	0.0000
IL8	0.0000	0.0000	0.0000	0.4200	0.4198	0.4200	0.4198	0.0000
Fas	0.0000	(0.0000)	0.0000	0.0048	0.0048	0.0048	0.0048	0.0702
COX2	0.0000	0.0000	0.0000	0.4200	0.4198	0.4200	0.4198	0.0000
TGF-β	0.0000	0.0000	0.0000	0.8349	0.8351	0.8349	0.8351	0.0000
IFN-γ	0.0000	0.0000	0.0000	0.1243	0.1240	0.1243	0.1240	0.0000
STAT3	0.0000	(0.0000)	0.0000	0.0702	0.0706	0.0702	0.0706	0.5745
GSK3β	1.0000	1.0000	1.0000	0.0309	0.0309	0.0309	0.0309	1.0000
Gastrin	0.0000	0.0000	0.0000	0.0000	0.9683	0.0000	0.9683	0.0000
Sox2	0.9638	0.0000	0.0000	0.9816	0.0001	0.9816	0.0001	0.9995
Cdx2	0.0000	0.0000	0.9638	0.0000	0.9836	0.0000	0.9836	0.0000
Shh	0.0292	0.0000	0.0000	0.9668	0.0000	0.9668	0.0000	0.0010

A (A_1, A_2 and A_3), R (R_1 and R_2), P (P_1 and P_2) are point attractors, D is a cyclic attractor. Dynamical trajectories of Caspase 8/10, Bid, Fas, VEGF/VEGFR, IL10, Ras and STAT3 is showed in Supplementary Figure S1.

Supplementary Table S9: Attractors of working endogenous network when *n* = 10, a = 1024

Components	A_1	A_2	A_3	R_1	R_2	P_1	P_2	D
Rb	1.0000	1.0000	1.0000	1.0000	0.0010	0.0010	0.0005	1.0000
Cyclin D/ Cdk4,6	0.0000	0.0000	(0.0000)	0.0010	0.9990	0.0010	0.9990	0.0000
Cyclin E/ Cdk2	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.9990	0.9990	0.0000
Myc	0.0000	0.0000	0.0000	0.0012	0.0012	0.0012	0.0012	0.0000
E2F	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.9990	0.9990	0.0000
p21	0.0000	0.0000	0.9990	0.0010	0.0010	0.0010	0.0010	0.9990
p27	0.9997	0.9995	0.9995	0.0010	0.0010	0.0005	0.0005	0.9997
p53	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0010	0.0010	0.9990
Caspase 3,7	0.0000	0.0000	(0.0000)	0.0001	0.0001	0.0001	0.0001	0.0010
Cytochrome c	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0005	0.0005	0.9997
Caspase 8,10	0.0000	0.0000	0.0000	0.3925	0.3925	0.3925	0.3925	0.2113
XIAP	0.0000	0.0000	0.0000	0.9990	0.9990	0.9990	0.9990	0.0000
Bcl-2	0.0000	0.0000	(0.0000)	0.0012	0.0012	0.0012	0.0012	0.0005
Bcl-xL	0.0000	0.0000	(0.0000)	0.9995	0.9995	0.9995	0.9995	0.0000
Bid	0.0000	0.0000	(0.0000)	0.0817	0.0816	0.0817	0.0816	0.5745
Bad	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.9990
Bax	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.9990
Ras	0.0000	0.0000	0.0000	0.9998	0.9998	0.9998	0.9998	0.9754
Akt	0.0010	0.0010	0.0010	0.9999	0.9999	0.9999	0.9999	0.0010
PTEN	1.0000	1.0000	1.0000	0.0010	0.0005	0.0010	0.0005	1.0000
ERK	0.0000	(0.0000)	(0.0000)	0.4677	0.4677	0.4677	0.4677	0.0010
JNK/p38	0.0000	0.0000	0.0000	0.4678	0.4677	0.4678	0.4677	0.0010
MKP	0.0000	0.0000	(0.0000)	0.5065	0.5065	0.5065	0.5065	0.0000
VEGF/ VEGFR	0.0000	0.0000	0.0000	0.9998	0.9998	0.9998	0.9998	0.9911
EGF/EGFR	0.0000	0.0000	0.0000	0.9990	0.9990	0.9990	0.9990	0.0000
IGF/IGFR	0.0000	0.0000	0.0000	0.9990	0.9990	0.9990	0.9990	0.0000
HGF/c-Met	0.0000	0.0000	0.0000	0.9990	0.9995	0.9990	0.9995	0.0000
Integrin/FAK	0.0000	(0.0000)	(0.0000)	0.9995	0.9995	0.9995	0.9995	0.0000
E-cadherin	1.0000	1.0000	1.0000	0.0003	0.0003	0.0003	0.0003	1.0000
Zeb1/2	0.0000	0.0000	(0.0000)	0.9988	0.9988	0.9988	0.9988	0.0000
β-catenin	0.0000	(0.0000)	0.0000	0.0010	0.9998	0.0010	0.9998	0.0000
HIF	0.0000	0.0000	0.0000	0.9990	0.9990	0.9990	0.9990	0.0000
NFκB	0.0000	(0.0000)	0.0000	0.3393	0.3392	0.3393	0.3392	0.0000
iκB	0.0000	0.0000	(0.0000)	0.0003	0.0003	0.0003	0.0003	0.0000

(*Continued*)

Components	A_1	A_2	A_3	R_1	R_2	P_1	P_2	D
TNF-α	0.0000	0.0000	(0.0000)	0.4770	0.4770	0.4770	0.4770	0.0000
IL10	0.0000	0.0000	0.0000	0.3844	0.3844	0.3844	0.3844	0.2113
IL1	0.0000	0.0000	(0.0000)	0.3408	0.3407	0.3408	0.3407	0.0000
IL8	0.0000	0.0000	(0.0000)	0.3482	0.3481	0.3482	0.3481	0.0000
Fas	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0702
COX2	0.0000	0.0000	(0.0000)	0.3482	0.3481	0.3482	0.3481	0.0000
TGF-β	0.0000	0.0000	0.0000	0.9793	0.9793	0.9793	0.9793	0.0000
IFN-γ	0.0000	0.0000	0.0000	0.0198	0.0197	0.0198	0.0197	0.0000
STAT3	0.0000	0.0000	0.0000	0.0012	0.0012	0.0012	0.0012	0.5745
GSK3β	1.0000	1.0000	1.0000	0.0010	0.0010	0.0010	0.0010	1.0000
Gastrin	(0.0000)	0.0000	(0.0000)	0.0000	0.9990	0.0000	0.9990	0.0000
Sox2	0.9990	0.0000	(0.0000)	0.9995	0.0000	0.9995	0.0000	0.9995
Cdx2	(0.0000)	0.0000	0.9990	0.0000	0.9995	0.0000	0.9995	0.0000
Shh	0.0010	(0.0000)	(0.0000)	0.9990	0.0000	0.9990	(0.0000)	0.0010

A (A_1, A_2 and A_3), R (R_1 and R_2), P (P_1 and P_2) are point attractors, D is a cyclic attractor. Dynamical trajectories of Caspase 8/10, Bid, Fas, VEGF/VEGFR, IL10, Ras and STAT3 is showed in Supplementary Figure S1.

Supplementary Table S10: Saddle points of working endogenous network when $n = 3$, a = 10

Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2
Rb	0.9713	0.2566	0.3048	0.1449	0.1070	0.2357	1.0000
Cyclin D/Cdk4,6	0.0682	0.1223	0.6066	0.8246	0.5952	0.6040	0.0000
Cyclin E/Cdk2	0.0466	0.6601	0.1654	0.3066	0.8542	0.4697	0.0000
Myc	0.2248	0.2611	0.2615	0.2634	0.2610	0.2612	0.0064
E2F	0.0095	0.5668	0.1295	0.2984	0.8446	0.4166	0.0000
p21	0.3934	0.0891	0.0883	0.0893	0.0902	0.0886	0.0000
p27	0.3875	0.0651	0.0675	0.0639	0.0436	0.0620	0.9479
p53	0.1183	0.0697	0.0391	0.0463	0.0841	0.0560	0.0000
Caspase 3,7	0.1363	0.0705	0.0704	0.0704	0.0704	0.0704	0.0000
Cytochrome c	0.1164	0.0452	0.0383	0.0394	0.0500	0.0415	0.0000
Caspase 8,10	0.3988	0.5272	0.5287	0.5290	0.5277	0.5285	0.0000
XIAP	0.5040	0.9056	0.9072	0.9076	0.9064	0.9070	0.0059
Bcl-2	0.2943	0.2496	0.2433	0.2432	0.2407	0.2428	0.0006
Bcl-xL	0.6838	0.7945	0.7944	0.7918	0.7946	0.7947	(0.0000)
Bid	0.3880	0.5943	0.5964	0.5969	0.5951	0.5961	(0.0000)
Bad	0.0074	0.0003	0.0001	0.0001	0.0005	0.0002	0.0000

(*Continued*)

Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2
Bax	0.0259	0.0249	0.0247	0.0254	0.0252	0.0248	0.0000
Ras	0.9152	0.9693	0.9702	0.9707	0.9702	0.9702	0.0000
Akt	0.4465	0.9730	0.9779	0.9798	0.9778	0.9779	0.0840
PTEN	0.4856	0.0934	0.0701	0.0556	0.0709	0.0703	0.9941
ERK	0.3193	0.3805	0.3826	0.3833	0.3826	0.3826	0.0000
JNK/p38	0.3265	0.3848	0.3853	0.3855	0.3853	0.3853	0.0000
MKP	0.4025	0.5285	0.5310	0.5318	0.5309	0.5310	0.0000
VEGF/VEGFR	0.8706	0.9721	0.9731	0.9735	0.9729	0.9730	0.0059
EGF/EGFR	0.4663	0.9030	0.9050	0.9058	0.9048	0.9049	0.0000
IGF/IGFR	0.5868	0.8781	0.8819	0.8815	0.8755	0.8805	0.0000
HGF/c-Met	0.6447	0.8887	0.9199	0.9381	0.9182	0.9195	0.0000
Integrin/FAK	0.3668	0.9274	0.9350	0.9385	0.9347	0.9350	(0.0000)
E-cadherin	0.1373	0.0483	0.0462	0.0450	0.0464	0.0462	1.0000
Zeb1/2	0.6598	0.7516	0.7523	0.7519	0.7500	0.7518	0.0000
β-catenin	0.1011	0.1314	0.6997	0.8921	0.6897	0.6974	(0.0000)
HIF	0.5288	0.9049	0.9086	0.9088	0.9037	0.9076	0.0059
NFκB	0.2513	0.3614	0.3633	0.3635	0.3614	0.3629	0.0000
iκB	0.1025	0.0441	0.0440	0.0438	0.0438	0.0439	0.0000
TNF-α	0.3557	0.4066	0.4073	0.4075	0.4069	0.4072	0.0000
IL10	0.3026	0.3711	0.3721	0.3723	0.3717	0.3720	0.0000
IL1	0.2772	0.3537	0.3545	0.3547	0.3539	0.3544	0.0000
IL8	0.3363	0.5102	0.5125	0.5130	0.5107	0.5121	0.0000
Fas	0.0193	0.0355	0.0356	0.0356	0.0355	0.0356	0.0000
COX2	0.3363	0.5102	0.5125	0.5130	0.5107	0.5121	0.0000
TGF-β	0.5727	0.6379	0.6354	0.6352	0.6384	0.6360	0.0000
IFNγ	0.1375	0.2030	0.2035	0.2035	0.2029	0.2033	0.0000
STAT3	0.2776	0.2606	0.2674	0.2690	0.2645	0.2667	(0.0000)
GSK3β	0.4881	0.0936	0.0923	0.0918	0.0924	0.0923	0.9941
Gastrin	0.0102	0.0222	0.7740	0.8765	0.7664	0.7723	0.0000
Sox2	0.8539	0.8554	0.3328	0.1960	0.3385	0.3342	0.4124
Cdx2	0.0014	0.0031	0.6240	0.8663	0.6106	0.6209	0.0000
Shh	0.3984	0.8552	0.0784	0.0093	0.0851	0.0799	0.0381

(*Continued*)

Components	S_8	S_9	S_{10}	S_{11}	S_{12}	S_{13}	S_{14}
Neighbor stable states	A_1,A_2	A_2,A_3	A_2,A_3	A_1,D	A_2,D	A_3,D	A_3,D
Rb	0.7654	0.9591	1.0000	0.7654	0.7654	0.9984	0.9834
Cyclin D/Cdk4,6	0.0000	0.0000	0.0000	0.0003	0.0000	0.0000	0.0003
Cyclin E/Cdk2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Myc	0.0027	0.0019	0.0035	0.0053	0.0024	0.0007	0.0010
E2F	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
p21	0.3115	0.5338	0.4102	0.3115	0.3115	0.8694	0.8679
p27	0.9336	0.9437	0.9464	0.9503	0.9309	0.9463	0.9554
p53	0.3571	0.3574	0.0000	0.3571	0.3571	0.3575	0.8832
Caspase 3,7	0.3129	0.1622	(0.0000)	0.3129	0.3129	0.0540	0.1190
Cytochrome c	0.3824	0.3828	(0.0000)	0.3824	0.3824	0.3829	0.9274
Caspase 8,10	0.2344	0.2354	(0.0000)	0.2344	0.2344	0.2356	0.4243
XIAP	0.0027	0.0036	0.0059	0.0027	0.0027	0.0038	0.0007
Bcl-2	0.0003	0.0001	0.0000	0.0029	0.0000	0.0001	0.0333
Bcl-xL	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
Bid	0.1141	0.1155	(0.0000)	0.1141	0.1141	0.1157	0.4330
Bad	0.3115	0.3117	(0.0000)	0.3115	0.3115	0.3117	0.8660
Bax	0.3128	0.3134	0.0000	0.3128	0.3128	0.3135	0.8729
Ras	0.0001	0.0001	0.0000	0.0001	0.0001	0.0001	0.4766
Akt	0.0752	0.0829	0.0840	0.0752	0.0752	0.0839	0.0850
PTEN	0.9958	0.9943	0.9941	0.9958	0.9958	0.9941	0.9939
ERK	0.0013	0.0014	(0.0000)	0.0013	0.0013	0.0014	0.0605
JNK/p38	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0441
MKP	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0031
VEGF/VEGFR	0.0188	0.0207	0.0059	0.0188	0.0188	0.0209	0.4499
EGF/EGFR	(0.0000)	(0.0000)	(0.0000)	0.0000	0.0000	(0.0000)	0.0000
IGF/IGFR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HGF/c-Met	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0022
Integrin/FAK	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
E-cadherin	0.7654	0.9591	1.0000	0.7654	0.7654	0.9984	0.9834
Zeb1/2	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
β-catenin	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
HIF	0.0029	0.0039	0.0059	0.0029	0.0029	0.0040	0.0008
NFκB	0.0000	0.0000	(0.0000)	0.0000	0.0000	(0.0000)	0.0001
iκB	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0018
TNF-α	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0017

(*Continued*)

IL10	0.2344	0.2354	(0.0000)	0.2344	0.2344	0.2356	0.4243
IL1	0.0000	0.0000	(0.0000)	0.0000	0.0000	(0.0000)	0.0009
IL8	0.0000	0.0000	(0.0000)	0.0000	0.0000	(0.0000)	0.0009
Fas	0.3128	0.3134	(0.0000)	0.3128	0.3128	0.3135	0.4192
COX2	0.0000	0.0000	(0.0000)	0.0000	0.0000	(0.0000)	0.0009
TGF-β	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
IFNγ	(0.0000)	(0.0000)	(0.0000)	0.0000	0.0000	(0.0000)	0.0000
STAT3	0.1141	0.1155	(0.0000)	0.1141	0.1141	0.1157	0.4330
GSK3β	0.9958	0.9943	0.9941	0.9958	0.9958	0.9941	0.9939
Gastrin	(0.0000)	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
Sox2	0.4055	0.0152	(0.0000)	0.8675	0.0147	0.0153	0.8860
Cdx2	(0.0000)	0.4126	0.4126	0.0000	0.0000	0.8669	0.0000
Shh	0.0368	0.0000	0.0000	0.0798	0.0000	0.0000	0.0808

Supplementary Table S11: Saddle points of working endogenous network when $n = 4$, a = 16

Components	**S_1**	**S_2**	**S_3**	**S_4**	**S_5**	**S_6**	**S_7**
Neighbor stable states	**A_1,R_1**	**R_1,P_1**	**R_1,R_2**	**R_2,P_2**	**P_1,P_2**	**R_1,R_2,P_1,P_2**	**A_1,A_2**
Rb	0.9997	0.2842	0.6196	0.0687	0.0767	0.2709	1.0000
Cyclin D/Cdk4,6	0.0444	0.0659	0.4426	0.9414	0.4426	0.4426	0.0000
Cyclin E/Cdk2	0.0462	0.6299	0.0090	0.4980	0.9192	0.6003	0.0000
Myc	0.2690	0.1557	0.1544	0.1562	0.1556	0.1546	0.0002
E2F	0.0045	0.5704	0.0027	0.4979	0.9187	0.5528	0.0000
p21	0.3722	0.0585	0.0583	0.0596	0.0595	0.0585	0.0000
p27	0.3890	0.0490	0.0509	0.0471	0.0303	0.0453	0.9704
p53	0.0659	0.0408	0.0135	0.0343	0.0566	0.0393	0.0000
Caspase 3,7	0.0587	0.0321	0.0321	0.0322	0.0321	0.0321	(0.0000)
Cytochrome c	0.0020	0.0241	0.0125	0.0211	0.0321	0.0234	0.0000
Caspase 8,10	0.3170	0.4672	0.4674	0.4680	0.4673	0.4673	(0.0000)
XIAP	0.5078	0.9395	0.9395	0.9396	0.9395	0.9395	0.0002
Bcl-2	0.3317	0.1538	0.1500	0.1502	0.1499	0.1500	0.0000
Bcl-xL	0.5746	0.9514	0.9517	0.9514	0.9514	0.9517	(0.0000)
Bid	0.1392	0.4325	0.4329	0.4341	0.4328	0.4329	(0.0000)
Bad	0.0001	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Bax	0.0264	0.0007	0.0006	0.0007	0.0007	0.0006	0.0000
Ras	0.9130	0.9813	0.9815	0.9821	0.9815	0.9815	0.0000
Akt	0.4958	0.9882	0.9883	0.9887	0.9883	0.9883	0.0554
PTEN	0.4922	0.0605	0.0550	0.0319	0.0550	0.0550	0.9998
ERK	0.3854	0.4311	0.4314	0.4324	0.4314	0.4314	0.0000
JNK/p38	0.3814	0.4335	0.4335	0.4336	0.4335	0.4335	0.0000
MKP	0.4089	0.5277	0.5282	0.5295	0.5282	0.5282	0.0000
VEGF/VEGFR	0.8369	0.9821	0.9822	0.9828	0.9822	0.9822	0.0002

(*Continued*)

Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2
EGF/EGFR	0.2783	0.9345	0.9347	0.9353	0.9347	0.9347	(0.0000)
IGF/IGFR	0.5524	0.9257	0.9258	0.9258	0.9256	0.9257	0.0000
HGF/c-Met	0.6137	0.9287	0.9362	0.9653	0.9362	0.9362	0.0000
Integrin/FAK	0.3625	0.9600	0.9606	0.9631	0.9606	0.9606	(0.0000)
E-cadherin	0.1632	0.0286	0.0282	0.0269	0.0282	0.0282	1.0000
Zeb1/2	0.6289	0.8470	0.8470	0.8467	0.8469	0.8469	(0.0000)
β-catenin	0.0577	0.0689	0.5667	0.9803	0.5667	0.5667	(0.0000)
HIF	0.5271	0.9395	0.9396	0.9396	0.9394	0.9395	0.0002
NFκB	0.2524	0.3609	0.3610	0.3613	0.3609	0.3610	0.0000
iκB	0.1061	0.0260	0.0260	0.0260	0.0260	0.0260	0.0000
TNF-α	0.3936	0.4418	0.4419	0.4422	0.4419	0.4419	0.0000
IL10	0.2773	0.3748	0.3750	0.3756	0.3750	0.3750	(0.0000)
IL1	0.2662	0.3594	0.3595	0.3597	0.3595	0.3595	0.0000
IL8	0.2876	0.4554	0.4555	0.4560	0.4555	0.4555	0.0000
Fas	0.0051	0.0139	0.0139	0.0139	0.0139	0.0139	0.0000
COX2	0.2876	0.4554	0.4555	0.4560	0.4555	0.4555	0.0000
TGF-β	0.5651	0.7574	0.7573	0.7569	0.7574	0.7573	0.0000
IFNγ	0.0679	0.1602	0.1602	0.1602	0.1601	0.1602	0.0000
STAT3	0.2702	0.1533	0.1540	0.1559	0.1540	0.1540	(0.0000)
GSK3β	0.4922	0.0605	0.0605	0.0604	0.0605	0.0605	0.9998
Gastrin	0.0002	0.0004	0.6226	0.9366	0.6226	0.6226	(0.0000)
Sox2	0.9267	0.9516	0.4606	0.0093	0.4606	0.4606	0.5000
Cdx2	0.0000	0.0000	0.3885	0.9664	0.3885	0.3885	(0.0000)
Shh	0.4753	0.9290	0.3067	0.0000	0.3067	0.3067	0.0294

Components	S_8	S_9	S_{10}	S_{11}	S_{12}	S_{13}	S_{14}
Neighbor stable states	A_1,A_2	A_2,A_3	A_2,A_3	A_1,D	A_2,D	A_3,D	A_3,D
Rb	0.8193	0.9935	1.0000	0.8193	0.8193	1.0000	0.9995
Cyclin D/Cdk4,6	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
Cyclin E/Cdk2	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
Myc	0.0001	0.0000	0.0001	0.0001	0.0001	0.0000	0.0000
E2F	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
p21	0.4111	0.6293	0.4999	0.4111	0.4111	0.9238	0.9232
p27	0.9602	0.9692	0.9695	0.9718	0.9586	0.9695	0.9775
p53	0.4571	0.4571	(0.0000)	0.4571	0.4571	0.4571	0.9314
Caspase 3,7	0.3427	0.1423	(0.0000)	0.3427	0.3427	0.0395	0.0741
Cytochrome c	0.4790	0.4790	(0.0000)	0.4790	0.4790	0.4790	0.9602

(*Continued*)

Components	S_8	S_9	S_{10}	S_{11}	S_{12}	S_{13}	S_{14}
Neighbor stable states	A_1,A_2	A_2,A_3	A_2,A_3	A_1,D	A_2,D	A_3,D	A_3,D
Caspase 8,10	0.3138	0.3138	(0.0000)	0.3138	0.3138	0.3138	0.4976
XIAP	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0000
Bcl-2	0.0000	0.0000	(0.0000)	0.0001	0.0000	0.0000	0.0195
Bcl-xL	(0.0000)	0.0000	(0.0000)	0.0000	0.0000	(0.0000)	0.0000
Bid	0.1342	0.1343	(0.0000)	0.1342	0.1342	0.1343	0.4951
Bad	0.4111	0.4111	0.0000	0.4111	0.4111	0.4111	0.9231
Bax	0.4112	0.4112	(0.0000)	0.4112	0.4112	0.4112	0.9233
Ras	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.4803
Akt	0.0517	0.0553	0.0554	0.0517	0.0517	0.0554	0.0557
PTEN	0.9999	0.9999	0.9999	0.9999	0.9999	0.9998	0.9998
ERK	0.0003	0.0003	0.0000	0.0003	0.0003	0.0003	0.0379
JNK/p38	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0283
MKP	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
VEGF/VEGFR	0.0053	0.0053	0.0001	0.0053	0.0053	0.0053	0.4902
EGF/EGFR	(0.0000)	(0.0000)	0.0000	(0.0000)	(0.0000)	0.0000	0.0000
IGF/IGFR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HGF/c-Met	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Integrin/FAK	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
E-cadherin	0.8193	0.9935	1.0000	0.8193	0.8193	1.0000	0.9995
Zeb1/2	(0.0000)	0.0000	(0.0000)	0.0000	0.0000	(0.0000)	0.0000
β-catenin	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
HIF	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0000
NFκB	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
iκB	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
TNF-α	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
IL10	0.3138	0.3138	(0.0000)	0.3138	0.3138	0.3138	0.4976
IL1	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
IL8	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
Fas	0.4112	0.4112	(0.0000)	0.4112	0.4112	0.4112	0.4988
COX2	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000
TGF-β	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
IFNγ	(0.0000)	(0.0000)	0.0000	(0.0000)	(0.0000)	(0.0000)	0.0000
STAT3	0.1342	0.1343	(0.0000)	0.1342	0.1342	0.1343	0.4951
GSK3β	0.9999	0.9999	0.9999	0.9999	0.9999	0.9998	0.9998
Gastrin	(0.0000)	(0.0000)	0.0000	(0.0000)	(0.0000)	0.0000	0.0000
Sox2	0.4987	0.0052	0.0000	0.9197	0.0052	0.0052	0.9276
Cdx2	(0.0000)	0.5000	0.5000	(0.0000)	(0.0000)	0.9196	0.0000
Shh	0.0293	0.0000	0.0000	0.0541	0.0000	0.0000	0.0543

Supplementary Table S12: Saddle points of working endogenous network when $n = 5$, a = 32

Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2
Rb	1.0000	0.3112	0.6682	0.0340	0.0356	0.2971	1.0000
Cyclin D/Cdk4,6	0.0217	0.0320	0.4347	0.9696	0.4347	0.4347	0.0000
Cyclin E/Cdk2	0.0247	0.5861	0.0001	0.5000	0.9638	0.5666	0.0000
Myc	0.2637	0.0707	0.0703	0.0706	0.0707	0.0704	0.0000
E2F	0.0012	0.5360	0.0000	0.5000	0.9638	0.5275	0.0000
p21	0.3778	0.0304	0.0304	0.0307	0.0307	0.0304	(0.0000)
p27	0.4034	0.0280	0.0285	0.0276	0.0157	0.0270	0.9848
p53	0.0335	0.0191	0.0047	0.0168	0.0300	0.0186	0.0000
Caspase 3,7	0.0232	0.0121	0.0121	0.0121	0.0121	0.0121	0.0000
Cytochrome c	0.0000	0.0103	0.0022	0.0090	0.0162	0.0100	0.0000
Caspase 8,10	0.2809	0.4387	0.4388	0.4389	0.4388	0.4388	(0.0000)
XIAP	0.5041	0.9691	0.9691	0.9691	0.9691	0.9691	0.0000
Bcl-2	0.3345	0.0703	0.0693	0.0692	0.0693	0.0693	0.0000
Bcl-xL	0.5664	0.9818	0.9818	0.9818	0.9818	0.9818	(0.0000)
Bid	0.0530	0.3422	0.3423	0.3426	0.3423	0.3423	(0.0000)
Bad	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	(0.0000)
Bax	0.0131	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Ras	0.9403	0.9913	0.9913	0.9915	0.9913	0.9913	0.0000
Akt	0.4986	0.9946	0.9946	0.9947	0.9946	0.9946	0.0294
PTEN	0.4959	0.0309	0.0293	0.0159	0.0293	0.0293	1.0000
ERK	0.4100	0.4420	0.4421	0.4425	0.4421	0.4421	0.0000
JNK/p38	0.4008	0.4432	0.4432	0.4431	0.4432	0.4432	0.0000
MKP	0.4123	0.5208	0.5209	0.5215	0.5209	0.5209	0.0000
VEGF/VEGFR	0.8349	0.9914	0.9914	0.9916	0.9914	0.9914	0.0000
EGF/EGFR	0.2034	0.9673	0.9673	0.9675	0.9673	0.9673	(0.0000)
IGF/IGFR	0.5344	0.9647	0.9647	0.9647	0.9647	0.9647	0.0000
HGF/c-Met	0.6029	0.9654	0.9674	0.9832	0.9674	0.9674	(0.0000)
Integrin/FAK	0.3670	0.9818	0.9819	0.9826	0.9819	0.9819	(0.0000)
E-cadherin	0.1378	0.0126	0.0125	0.0122	0.0125	0.0125	1.0000
Zeb1/2	0.6408	0.9294	0.9294	0.9295	0.9294	0.9294	(0.0000)
β-catenin	0.0277	0.0328	0.5631	0.9910	0.5631	0.5631	(0.0000)
HIF	0.5140	0.9691	0.9691	0.9691	0.9691	0.9691	0.0000
NFκB	0.2486	0.3536	0.3536	0.3535	0.3536	0.3536	0.0000
iκB	0.1023	0.0122	0.0122	0.0122	0.0122	0.0122	0.0000

(*Continued*)

Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2
TNF-α	0.4065	0.4515	0.4515	0.4516	0.4515	0.4515	0.0000
IL10	0.2621	0.3747	0.3748	0.3750	0.3748	0.3748	(0.0000)
IL1	0.2564	0.3554	0.3554	0.3553	0.3554	0.3554	0.0000
IL8	0.2654	0.4200	0.4199	0.4198	0.4199	0.4199	0.0000
Fas	0.0012	0.0048	0.0048	0.0048	0.0048	0.0048	(0.0000)
COX2	0.2654	0.4200	0.4199	0.4198	0.4199	0.4199	0.0000
TGF-β	0.5594	0.8349	0.8350	0.8351	0.8350	0.8350	0.0000
IFNγ	0.0329	0.1243	0.1242	0.1240	0.1242	0.1242	(0.0000)
STAT3	0.2623	0.0702	0.0703	0.0706	0.0703	0.0703	(0.0000)
GSK3β	0.4959	0.0309	0.0309	0.0309	0.0309	0.0309	1.0000
Gastrin	0.0000	0.0000	0.6443	0.9683	0.6443	0.6443	0.0000
Sox2	0.9652	0.9816	0.4727	0.0001	0.4727	0.4727	0.5000
Cdx2	0.0000	0.0000	0.3848	0.9836	0.3848	0.3848	(0.0000)
Shh	0.4920	0.9668	0.3388	0.0000	0.3388	0.3388	0.0152

Components	S_8	S_9	S_{10}	S_{11}	S_{12}	S_{13}	S_{14}
Neighbor stable states	A_1,A_2	A_2,A_3	A_2,A_3	A_1,D	A_2,D	A_3,D	A_3,D
Rb	0.8729	0.9994	1.0000	0.8729	0.8729	1.0000	1.0000
Cyclin D/Cdk4,6	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Cyclin E/Cdk2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Myc	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
E2F	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
p21	0.4316	0.6376	0.5000	0.4316	0.4316	0.9647	0.9643
p27	0.9801	0.9846	0.9846	0.9868	0.9797	0.9846	0.9891
p53	0.4732	0.4732	0.0000	0.4732	0.4732	0.4732	0.9669
Caspase 3,7	0.3401	0.1151	0.0000	0.3401	0.3401	0.0181	0.0350
Cytochrome c	0.4894	0.4894	0.0000	0.4894	0.4894	0.4894	0.9819
Caspase 8,10	0.3239	0.3239	0.0000	0.3239	0.3239	0.3239	0.4995
XIAP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Bcl-2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0090
Bcl-xL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	(0.0000)
Bid	0.1024	0.1024	0.0000	0.1024	0.1024	0.1024	0.4988
Bad	0.4316	0.4316	0.0000	0.4316	0.4316	0.4316	0.9643
Bax	0.4316	0.4316	0.0000	0.4316	0.4316	0.4316	0.9643
Ras	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.4927

(*Continued*)

Components	S_8	S_9	S_{10}	S_{11}	S_{12}	S_{13}	S_{14}
Neighbor stable states	**A_1,A_2**	**A_2,A_3**	**A_2,A_3**	**A_1,D**	**A_2,D**	**A_3,D**	**A_3,D**
Akt	0.0285	0.0294	0.0294	0.0285	0.0285	0.0294	0.0294
PTEN	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
ERK	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0199
JNK/p38	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0149
MKP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
VEGF/VEGFR	0.0004	0.0004	0.0000	0.0004	0.0004	0.0004	0.4971
EGF/EGFR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
IGF/IGFR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HGF/c-Met	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Integrin/FAK	0.0000	0.0000	0.0000	(0.0000)	(0.0000)	0.0000	0.0000
E-cadherin	0.8729	0.9994	1.0000	0.8729	0.8729	1.0000	1.0000
Zeb1/2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	(0.0000)
β-catenin	0.0000	(0.0000)	0.0000	(0.0000)	(0.0000)	0.0000	0.0000
HIF	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
NFκB	0.0000	0.0000	0.0000	(0.0000)	(0.0000)	0.0000	0.0000
iκB	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TNF-α	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
IL10	0.3239	0.3239	0.0000	0.3239	0.3239	0.3239	0.4995
IL1	0.0000	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000
IL8	0.0000	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000
Fas	0.4316	0.4316	0.0000	0.4316	0.4316	0.4316	0.4998
COX2	0.0000	0.0000	0.0000	(0.0000)	0.0000	0.0000	0.0000
TGF-β	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
IFNγ	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
STAT3	0.1024	0.1024	0.0000	0.1024	0.1024	0.1024	0.4988
GSK3β	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
Gastrin	0.0000	0.0000	0.0000	0.0000	0.0000	(0.0000)	0.0000
Sox2	0.4999	0.0004	0.0000	0.9638	0.0004	0.0004	0.9653
Cdx2	0.0000	0.5000	0.5000	0.0000	0.0000	0.9638	0.0000
Shh	0.0151	0.0000	0.0000	0.0292	0.0000	0.0000	0.0292

Supplementary Table S13: Saddle points of working endogenous network when $n = 10$, a = 1024

Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2
Rb	1.0000	0.3663	0.8118	0.0010	0.0010	0.3585	1.0000
Cyclin D/Cdk4,6	0.0006	0.0010	0.4320	0.9990	0.4320	0.4320	0.0000
Cyclin E/Cdk2	0.0015	0.5282	0.0000	0.5000	0.9990	0.5227	0.0000
Myc	0.2664	0.0012	0.0012	0.0012	0.0012	0.0012	0.0000
E2F	0.0000	0.5057	0.0000	0.5000	0.9990	0.5046	0.0000
p21	0.3832	0.0010	0.0010	0.0010	0.0010	0.0010	(0.0000)
p27	0.4202	0.0010	0.0010	0.0010	0.0005	0.0010	0.9995
p53	0.0019	0.0005	0.0000	0.0005	0.0010	0.0005	0.0000
Caspase 3,7	0.0000	0.0001	0.0001	0.0001	0.0001	0.0001	(0.0000)
Cytochrome c	0.0000	0.0003	0.0000	0.0002	0.0005	0.0003	0.0000
Caspase 8,10	0.1728	0.3925	0.3925	0.3925	0.3925	0.3925	(0.0000)
XIAP	0.5001	0.9990	0.9990	0.9990	0.9990	0.9990	0.0000
Bcl-2	0.3440	0.0012	0.0012	0.0012	0.0012	0.0012	0.0000
Bcl-xL	0.5126	0.9995	0.9995	0.9995	0.9995	0.9995	0.0000
Bid	0.0000	0.0817	0.0817	0.0816	0.0817	0.0817	(0.0000)
Bad	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Bax	0.0008	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Ras	0.9961	0.9998	0.9998	0.9998	0.9998	0.9998	0.0000
Akt	0.4999	0.9999	0.9999	0.9999	0.9999	0.9999	0.0010
PTEN	0.4999	0.0010	0.0010	0.0005	0.0010	0.0010	1.0000
ERK	0.4536	0.4677	0.4677	0.4677	0.4677	0.4677	0.0000
JNK/p38	0.4522	0.4678	0.4678	0.4677	0.4678	0.4678	0.0000
MKP	0.4265	0.5065	0.5065	0.5065	0.5065	0.5065	(0.0000)
VEGF/VEGFR	0.8694	0.9998	0.9998	0.9998	0.9998	0.9998	0.0000
EGF/EGFR	0.1209	0.9990	0.9990	0.9990	0.9990	0.9990	(0.0000)
IGF/IGFR	0.5026	0.9990	0.9990	0.9990	0.9990	0.9990	0.0000
HGF/c-Met	0.5812	0.9990	0.9990	0.9995	0.9990	0.9990	(0.0000)
Integrin/FAK	0.4094	0.9995	0.9995	0.9995	0.9995	0.9995	(0.0000)
E-cadherin	0.0489	0.0003	0.0003	0.0003	0.0003	0.0003	1.0000
Zeb1/2	0.6546	0.9988	0.9988	0.9988	0.9988	0.9988	0.0000
β-catenin	0.0008	0.0010	0.5484	0.9998	0.5484	0.5484	(0.0000)
HIF	0.5005	0.9990	0.9990	0.9990	0.9990	0.9990	0.0000
NFκB	0.2682	0.3393	0.3393	0.3392	0.3393	0.3393	0.0000
iκB	0.1042	0.0003	0.0003	0.0003	0.0003	0.0003	(0.0000)
TNF-α	0.4271	0.4770	0.4770	0.4770	0.4770	0.4770	(0.0000)

(*Continued*)

Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2
IL10	0.1714	0.3844	0.3844	0.3844	0.3844	0.3844	(0.0000)
IL1	0.2687	0.3408	0.3408	0.3407	0.3408	0.3408	0.0000
IL8	0.2692	0.3482	0.3482	0.3481	0.3482	0.3482	0.0000
Fas	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COX2	0.2692	0.3482	0.3482	0.3481	0.3482	0.3482	0.0000
TGF-β	0.5330	0.9793	0.9793	0.9793	0.9793	0.9793	0.0000
IFNγ	0.0020	0.0198	0.0198	0.0197	0.0198	0.0198	0.0000
STAT3	0.2828	0.0012	0.0012	0.0012	0.0012	0.0012	(0.0000)
GSK3β	0.4999	0.0010	0.0010	0.0010	0.0010	0.0010	1.0000
Gastrin	0.0000	0.0000	0.7159	0.9990	0.7159	0.7159	(0.0000)
Sox2	0.9990	0.9995	0.4903	0.0000	0.4903	0.4903	0.5000
Cdx2	0.0000	0.0000	0.3970	0.9995	0.3970	0.3970	(0.0000)
Shh	0.4998	0.9990	0.4105	0.0000	0.4105	0.4105	0.0005

Components	S_8	S_9	S_{10}	S_{11}	S_{12}	S_{13}	S_{14}
Neighbor stable states	A_1,A_2	A_2,A_3	A_2,A_3	A_1,D	A_2,D	A_3,D	A_3,D
Rb	0.9835	1.0000	1.0000	0.9835	0.9835	1.0000	1.0000
Cyclin D/Cdk4,6	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000	0.0000
Cyclin E/Cdk2	(0.0000)	0.0000	0.0000	0.0000	(0.0000)	0.0000	0.0000
Myc	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
E2F	(0.0000)	0.0000	0.0000	0.0000	(0.0000)	0.0000	0.0000
p21	0.4663	0.5000	0.6520	0.4663	0.4663	0.9990	0.9990
p27	0.9995	0.9995	0.9995	0.9997	0.9995	0.9995	0.9997
p53	0.4933	0.0000	0.4933	0.4933	0.4933	0.4933	0.9990
Caspase 3,7	0.3323	0.0000	0.0327	0.3323	0.3323	0.0005	0.0010
Cytochrome c	0.4987	(0.0000)	0.4987	0.4987	0.4987	0.4987	0.9995
Caspase 8,10	0.3321	0.0000	0.3321	0.3321	0.3321	0.3321	0.5000
XIAP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Bcl-2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0002
Bcl-xL	(0.0000)	0.0000	(0.0000)	0.0000	0.0000	(0.0000)	0.0000
Bid	0.0165	0.0000	0.0165	0.0165	0.0165	0.0165	0.5000
Bad	0.4663	0.0000	0.4663	0.4663	0.4663	0.4663	0.9990
Bax	0.4663	0.0000	0.4663	0.4663	0.4663	0.4663	0.9990
Ras	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.4999
Akt	0.0010	0.0010	0.0010	0.0010	0.0010	0.0010	0.0010

(*Continued*)

Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2
PTEN	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
ERK	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0007
JNK/p38	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0005
MKP	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000	0.0000
VEGF/VEGFR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.5000
EGF/EGFR	0.0000	0.0000	0.0000	0.0000	0.0000	(0.0000)	0.0000
IGF/IGFR	(0.0000)	0.0000	0.0000	0.0000	(0.0000)	0.0000	(0.0000)
HGF/c-Met	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000	0.0000
Integrin/FAK	(0.0000)	0.0000	0.0000	0.0000	(0.0000)	0.0000	0.0000
E-cadherin	0.9835	1.0000	1.0000	0.9835	0.9835	1.0000	1.0000
Zeb1/2	0.0000	0.0000	(0.0000)	0.0000	0.0000	(0.0000)	0.0000
β-catenin	(0.0000)	0.0000	0.0000	0.0000	(0.0000)	0.0000	0.0000
HIF	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
NFκB	0.0000	(0.0000)	0.0000	0.0000	(0.0000)	0.0000	0.0000
iκB	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000	0.0000
TNF-α	0.0000	(0.0000)	0.0000	0.0000	0.0000	0.0000	0.0000
IL10	0.3321	0.0000	0.3321	0.3321	0.3321	0.3321	0.5000
IL1	0.0000	(0.0000)	0.0000	0.0000	0.0000	(0.0000)	0.0000
IL8	0.0000	(0.0000)	0.0000	0.0000	0.0000	(0.0000)	0.0000
Fas	0.4663	0.0000	0.4663	0.4663	0.4663	0.4663	0.5000
COX2	0.0000	(0.0000)	0.0000	0.0000	0.0000	(0.0000)	0.0000
TGF-β	(0.0000)	0.0000	0.0000	0.0000	(0.0000)	0.0000	(0.0000)
IFNγ	(0.0000)	0.0000	0.0000	(0.0000)	0.0000	(0.0000)	0.0000
STAT3	0.0165	0.0000	0.0165	0.0165	0.0165	0.0165	0.5000
GSK3β	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
Gastrin	(0.0000)	(0.0000)	(0.0000)	0.0000	(0.0000)	(0.0000)	(0.0000)
Sox2	0.5000	(0.0000)	0.0000	0.9990	0.0000	0.0000	0.9990
Cdx2	0.0000	0.5000	0.5000	0.0000	(0.0000)	0.9990	(0.0000)
Shh	0.0005	(0.0000)	0.0000	0.0010	0.0000	0.0000	0.0010

Supplementary Table S14: Invariant point attractors of ordinary differential equations (ODE) model under random parameter $n_i (3 \leq n_i \leq 10; i = 1, 2, ..., 215)$ and $a_i = 2^{n_i}$ and parameter $n = 3$, $a = 10$

	Random Parameter n_i=[3,10], $a=2^{n_i}$, i=1,2,…,215.							Parameter n=3,a=10						
	A_1	A_2	A_3	R_1	R_2	P_1	P_2	A_1	A_2	A_3	R_1	R_2	P_1	P_2
Rb	1.00	1.00	1.00	1.00	0.00	0.00	0.00	1.00	1.00	1.00	0.95	0.15	0.14	0.08
Cyclin D/Cdk4,6	0.00	(0.00)	0.00	0.00	0.99	0.00	0.99	0.00	0.00	0.00	0.12	0.82	0.12	0.83
Cyclin E/Cdk2	0.00	(0.00)	0.00	0.00	0.00	0.99	0.99	0.00	0.00	0.00	0.15	0.21	0.84	0.86
Myc	0.00	0.00	(0.00)	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.26	0.26	0.26	0.26
E2F	0.00	(0.00)	0.00	0.00	0.00	0.99	0.99	0.00	0.00	0.00	0.02	0.20	0.82	0.86
p21	0.00	0.00	1.00	0.01	0.01	0.01	0.01	0.00	0.00	0.86	0.09	0.09	0.09	0.09
p27	0.99	0.99	0.99	0.00	0.00	0.00	0.00	0.96	0.95	0.95	0.08	0.07	0.05	0.04
p53	(0.00)	(0.00)	0.00	0.00	0.00	0.06	0.06	0.00	0.00	0.00	0.04	0.04	0.08	0.08
Caspase 3,7	(0.00)	(0.00)	(0.00)	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.07	0.07	0.07	0.07
Cytochrome *c*	0.00	0.00	(0.00)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.04	0.05	0.05
Caspase 8,10	(0.00)	(0.00)	0.00	0.49	0.49	0.49	0.49	0.00	0.00	0.00	0.53	0.53	0.53	0.53
XIAP	0.00	0.00	0.00	0.94	0.94	0.94	0.94	0.01	0.01	0.01	0.91	0.91	0.91	0.91
Bcl-2	0.00	0.00	(0.00)	0.08	0.07	0.08	0.07	0.01	0.00	0.00	0.25	0.24	0.25	0.24
Bcl-xL	(0.00)	(0.00)	0.00	0.99	0.99	0.99	0.99	0.00	0.00	0.00	0.79	0.79	0.79	0.79
Bid	0.00	(0.00)	0.00	0.44	0.45	0.44	0.45	0.00	0.00	0.00	0.60	0.60	0.59	0.60
Bad	(0.00)	0.00	(0.00)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bax	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.03	0.03	0.03
Ras	(0.00)	(0.00)	0.00	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.97	0.97	0.97	0.97
Akt	0.01	0.01	0.01	1.00	1.00	1.00	1.00	0.08	0.08	0.08	0.97	0.98	0.97	0.98
PTEN	1.00	1.00	1.00	0.03	0.00	0.03	0.00	0.99	0.99	0.99	0.09	0.06	0.09	0.06
ERK	0.00	0.00	(0.00)	0.48	0.48	0.48	0.48	0.00	0.00	0.00	0.38	0.38	0.38	0.38
JNK/p38	0.00	0.00	(0.00)	0.45	0.45	0.45	0.45	0.00	0.00	0.00	0.38	0.39	0.38	0.39
MKP	0.00	(0.00)	0.00	0.51	0.51	0.51	0.51	0.00	0.00	0.00	0.53	0.53	0.53	0.53
VEGF/VEGFR	0.00	0.00	0.00	1.00	1.00	1.00	1.00	0.01	0.01	0.01	0.97	0.97	0.97	0.97
EGF/EGFR	(0.00)	0.00	0.00	0.94	0.94	0.94	0.94	0.00	0.00	0.00	0.90	0.91	0.90	0.91
IGF/IGFR	0.00	(0.00)	(0.00)	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.88	0.88	0.88	0.88
HGF/c-Met	0.00	0.00	0.00	0.93	1.00	0.93	1.00	0.00	0.00	0.00	0.89	0.94	0.89	0.94
Integrin/FAK	(0.00)	0.00	(0.00)	0.99	0.99	0.99	0.99	0.00	0.00	0.00	0.93	0.94	0.93	0.94
E-cadherin	1.00	1.00	1.00	0.01	0.01	0.01	0.01	1.00	1.00	1.00	0.05	0.04	0.05	0.05
Zeb1/2	(0.00)	(0.00)	0.00	0.94	0.93	0.93	0.93	0.00	0.00	0.00	0.75	0.75	0.75	0.75
β-catenin	0.00	0.00	(0.00)	0.02	1.00	0.02	1.00	0.00	0.00	0.00	0.13	0.89	0.13	0.90
HIF	0.00	0.00	0.00	0.93	0.93	0.93	0.93	0.01	0.01	0.01	0.91	0.91	0.90	0.90
NFκB	0.00	0.00	(0.00)	0.35	0.36	0.35	0.36	0.00	0.00	0.00	0.36	0.36	0.36	0.36
ikB	0.00	0.00	0.00	0.02	0.02	0.02	0.02	0.00	0.00	0.00	0.04	0.04	0.04	0.04
TNF-α	(0.00)	0.00	0.00	0.48	0.48	0.48	0.48	0.00	0.00	0.00	0.41	0.41	0.41	0.41
IL10	(0.00)	(0.00)	0.00	0.43	0.43	0.43	0.43	0.00	0.00	0.00	0.37	0.37	0.37	0.37
IL1	(0.00)	(0.00)	(0.00)	0.33	0.33	0.33	0.33	0.00	0.00	0.00	0.35	0.35	0.35	0.35
IL8	0.00	0.00	(0.00)	0.42	0.42	0.42	0.42	0.00	0.00	0.00	0.51	0.51	0.51	0.51
FasL	(0.00)	0.00	(0.00)	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.04	0.04	0.04	0.04
COX2	0.00	(0.00)	(0.00)	0.31	0.32	0.31	0.32	0.00	0.00	0.00	0.51	0.51	0.51	0.51
TGF-β	0.00	0.00	0.00	0.88	0.88	0.88	0.88	0.00	0.00	0.00	0.64	0.64	0.64	0.64
IFNγ	(0.00)	(0.00)	0.00	0.07	0.08	0.07	0.08	0.00	0.00	0.00	0.20	0.20	0.20	0.20
STAT3	(0.00)	(0.00)	0.00	0.04	0.04	0.04	0.04	0.00	0.00	0.00	0.26	0.27	0.26	0.27
GSK3β	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.99	0.99	0.99	0.09	0.09	0.09	0.09
Gastrin	0.00	0.00	0.00	0.00	0.98	0.00	0.98	0.00	0.00	0.00	0.02	0.88	0.02	0.88
Sox2	1.00	(0.00)	0.00	1.00	0.00	1.00	0.00	0.87	0.00	0.00	0.86	0.20	0.86	0.19
Cdx2	0.00	0.00	0.94	0.00	0.99	0.00	0.99	0.00	0.00	0.87	0.00	0.87	0.00	0.88
Shh	0.00	(0.00)	(0.00)	0.99	0.00	0.99	0.00	0.08	0.00	0.00	0.86	0.01	0.86	0.01

Supplementary Table S15: Invariant saddle points of working endogenous network under random parameter $n_i (3 \leq n_i \leq 10; i = 1, 2, ..., 215)$ and $a_i = 2^{n_i}$

Random Parameter n_i=[3,10], $a=2^{n_i}$, i=1,2,…,215.														
Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7	S_8	S_9	S_{10}	S_{11}	S_{12}	S_{13}	S_{14}
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2	A_1,A_2	A_2,A_3	A_2,A_3	A_1,D	A_2,D	A_3,D	A_3,D
Rb	0.99	0.22	0.81	0.00	0.00	0.27	0.86	1.00	1.00	1.00	0.86	0.86	1.00	1.00
Cyclin D/Cdk4,6	0.00	0.00	0.42	0.99	0.42	0.42	0.00	0.00	(0.00)	0.00	0.00	0.00	0.00	0.00
Cyclin E/Cdk2	0.01	0.55	0.00	0.50	0.99	0.55	0.00	0.00	(0.00)	0.00	(0.00)	(0.00)	0.00	0.00
Myc	0.33	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
E2F	0.00	0.52	0.00	0.50	0.99	0.52	0.00	0.00	0.00	(0.00)	0.00	(0.00)	0.00	0.00
p21	0.35	0.01	0.01	0.01	0.01	0.01	0.45	0.00	0.50	0.65	0.45	0.45	1.00	0.96
p27	0.08	0.00	0.00	0.00	0.00	0.00	0.98	0.99	0.99	0.99	0.99	0.98	0.99	0.99
p53	0.07	0.04	0.00	0.03	0.06	0.04	0.48	0.00	(0.00)	0.48	0.48	0.48	0.48	0.95
Caspase 3,7	0.17	0.01	0.01	0.03	0.01	0.01	0.31	(0.00)	0.00	0.07	0.31	0.31	0.00	0.01
Cytochrome *c*	0.09	0.00	0.00	0.00	0.00	0.00	0.49	(0.00)	0.00	0.49	0.49	0.49	0.49	1.00
Caspase 8,10	0.48	0.49	0.49	0.99	0.49	0.49	0.26	0.00	(0.00)	0.26	0.26	0.26	0.26	0.51
XIAP	0.53	0.94	0.94	0.94	0.94	0.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bcl-2	0.44	0.08	0.07	0.07	0.07	0.07	0.00	0.00	0.00	(0.00)	0.00	0.00	0.00	0.01
Bcl-xL	0.72	0.99	0.99	0.99	0.99	0.99	0.00	0.00	0.00	0.00	0.00	(0.00)	(0.00)	0.00
Bid	0.42	0.44	0.44	1.00	0.44	0.44	0.00	(0.00)	0.00	0.00	0.00	0.00	0.00	0.56
Bad	0.00	0.00	0.00	0.00	0.00	0.00	0.45	0.00	(0.00)	0.45	0.45	0.45	0.45	0.96
Bax	0.02	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.44	0.44	0.44	0.44	0.99
Ras	1.00	1.00	1.00	1.00	1.00	1.00	0.00	(0.00)	0.00	0.00	0.00	0.00	0.00	0.74
Akt	0.49	1.00	1.00	1.00	1.00	1.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
PTEN	0.50	0.03	0.03	0.00	0.03	0.03	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
ERK	0.42	0.48	0.48	0.48	0.48	0.48	0.00	0.00	(0.00)	0.00	0.00	0.00	0.00	0.00
JNK/p38	0.46	0.45	0.45	0.45	0.45	0.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07
MKP	0.39	0.51	0.51	0.51	0.51	0.51	0.00	(0.00)	0.00	0.00	0.00	0.00	(0.00)	0.00
VEGF/VEGFR	0.89	1.00	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.56
EGF/EGFR	0.47	0.94	0.94	0.94	0.94	0.94	(0.00)	0.00	(0.00)	(0.00)	0.00	0.00	0.00	0.00
IGF/IGFR	0.59	1.00	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
HGF/c-Met	0.59	0.93	0.94	1.00	0.94	0.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Integrin/FAK	0.38	0.99	0.99	0.99	0.99	0.99	0.00	0.00	0.00	0.00	0.00	(0.00)	0.00	0.00
E-cadherin	0.19	0.01	0.01	0.01	0.01	0.01	0.88	1.00	1.00	1.00	0.88	0.88	1.00	1.00
Zeb1/2	0.56	0.94	0.94	0.93	0.93	0.94	0.00	(0.00)	(0.00)	0.00	(0.00)	0.00	(0.00)	0.00
β-catenin	0.02	0.02	0.53	1.00	0.53	0.53	0.00	0.00	0.00	0.00	0.00	(0.00)	0.00	0.00
HIF	0.52	0.93	0.93	0.93	0.93	0.93	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NFκB	0.37	0.35	0.35	0.36	0.35	0.35	0.00	(0.00)	0.00	(0.00)	0.00	(0.00)	(0.00)	0.00
iκB	0.11	0.02	0.02	0.01	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
TNF-α	0.48	0.48	0.48	0.61	0.48	0.48	0.00	0.00	(0.00)	0.00	0.00	0.00	(0.00)	0.00
IL10	0.41	0.43	0.43	0.43	0.43	0.43	0.34	0.00	(0.00)	0.34	0.34	0.34	0.34	0.51
IL1	0.34	0.33	0.33	0.33	0.33	0.33	0.00	(0.00)	(0.00)	(0.00)	0.00	(0.00)	(0.00)	0.00
IL8	0.43	0.42	0.42	0.42	0.42	0.42	0.00	0.00	0.00	(0.00)	0.00	0.00	0.00	0.00
FasL	0.01	0.01	0.01	0.05	0.01	0.01	0.45	(0.00)	(0.00)	0.45	0.45	0.45	0.45	0.50
COX2	0.34	0.31	0.31	0.32	0.31	0.31	0.00	(0.00)	0.00	(0.00)	(0.00)	0.00	(0.00)	0.00
TGF-β	0.51	0.88	0.88	0.88	0.88	0.88	0.00	(0.00)	0.00	0.00	0.00	0.00	0.00	0.00
IFNγ	0.10	0.07	0.07	0.51	0.07	0.07	0.00	0.00	(0.00)	0.00	0.00	0.00	(0.00)	0.00
STAT3	0.38	0.04	0.04	0.04	0.04	0.04	0.07	0.00	0.00	0.07	0.07	0.07	0.07	0.52
GSK3β	0.51	0.00	0.00	0.00	0.00	0.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Gastrin	0.00	0.00	0.58	0.98	0.58	0.58	0.00	0.00	0.00	0.00	(0.00)	0.00	(0.00)	0.00
Sox2	1.00	1.00	0.49	0.00	0.49	0.49	0.34	0.50	(0.00)	0.00	1.00	0.00	0.00	1.00
Cdx2	0.00	0.00	0.33	0.99	0.33	0.33	(0.00)	0.00	0.50	0.50	0.00	0.00	0.94	0.00
Shh	0.43	0.99	0.41	(0.00)	0.41	0.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Supplementary Table S16: Invariant point attractors of ordinary differential equations (ODE) model under random parameter $n_i(3 \leq n_i \leq 10; i = 1, 2, ..., 215)$ and $a_i = 2^{n_i}$ and parameter $n = 3$, $a = 10$

	Random Parameter n_i=[1,10], $a=2^{ni}$, i=1,2,…,215.							Parameter n=3,a=10						
	A_1	A_2	A_3	R_1	R_2	P_1	P_2	A_1	A_2	A_3	R_1	R_2	P_1	P_2
Rb	1.00	1.00	1.00	1.00	0.02	0.01	0.00	1.00	1.00	1.00	0.95	0.15	0.14	0.08
Cyclin D/Cdk4,6	0.00	0.00	0.00	0.03	1.00	0.03	1.00	0.00	0.00	0.00	0.12	0.82	0.12	0.83
Cyclin E/Cdk2	0.00	0.00	0.00	0.00	0.00	1.00	1.00	0.00	0.00	0.00	0.15	0.21	0.84	0.86
Myc	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.26	0.26	0.26	0.26
E2F	0.00	0.00	0.00	0.00	0.00	0.98	0.98	0.00	0.00	0.00	0.02	0.20	0.82	0.86
p21	0.00	0.00	1.00	0.07	0.07	0.07	0.07	0.00	0.00	0.86	0.09	0.09	0.09	0.09
p27	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.96	0.95	0.95	0.08	0.07	0.05	0.04
p53	0.00	0.00	0.00	0.01	0.01	0.04	0.04	0.00	0.00	0.00	0.04	0.04	0.08	0.08
Caspase 3,7	0.00	0.00	0.00	0.05	0.05	0.05	0.05	0.00	0.00	0.00	0.07	0.07	0.07	0.07
Cytochrome *c*	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.04	0.04	0.05	0.05
Caspase 8,10	0.00	0.00	0.00	0.49	0.49	0.49	0.49	0.00	0.00	0.00	0.53	0.53	0.53	0.53
XIAP	0.00	0.00	0.00	0.92	0.92	0.92	0.92	0.01	0.01	0.01	0.91	0.91	0.91	0.91
Bcl-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.25	0.24	0.25	0.24
Bcl-xL	0.00	0.00	0.00	0.98	0.98	0.98	0.98	0.00	0.00	0.00	0.79	0.79	0.79	0.79
Bid	0.00	0.00	0.00	0.49	0.49	0.49	0.49	0.00	0.00	0.00	0.60	0.60	0.59	0.60
Bad	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bax	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.03	0.03	0.03
Ras	0.00	0.00	0.00	0.98	0.98	0.98	0.98	0.00	0.00	0.00	0.97	0.97	0.97	0.97
Akt	0.04	0.04	0.04	1.00	1.00	1.00	1.00	0.08	0.08	0.08	0.97	0.98	0.97	0.98
PTEN	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.99	0.99	0.99	0.09	0.06	0.09	0.06
ERK	0.00	0.00	0.00	0.45	0.45	0.45	0.45	0.00	0.00	0.00	0.38	0.38	0.38	0.38
JNK/p38	0.00	0.00	0.00	0.45	0.45	0.45	0.45	0.00	0.00	0.00	0.38	0.39	0.38	0.39
MKP	0.00	0.00	0.00	0.51	0.51	0.51	0.51	0.00	0.00	0.00	0.53	0.53	0.53	0.53
VEGF/VEGFR	0.00	0.00	0.00	1.00	1.00	1.00	1.00	0.01	0.01	0.01	0.97	0.97	0.97	0.97
EGF/EGFR	0.00	0.00	0.00	0.98	0.98	0.98	0.98	0.00	0.00	0.00	0.90	0.91	0.90	0.91
IGF/IGFR	0.00	0.00	0.00	0.98	0.98	0.98	0.98	0.00	0.00	0.00	0.88	0.88	0.88	0.88
HGF/c-Met	0.00	0.00	0.00	0.95	0.97	0.95	0.97	0.00	0.00	0.00	0.89	0.94	0.89	0.94
Integrin/FAK	0.00	0.00	0.00	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.93	0.94	0.93	0.94
E-cadherin	1.00	1.00	1.00	0.01	0.01	0.01	0.01	1.00	1.00	1.00	0.05	0.04	0.05	0.05
Zeb1/2	0.00	0.00	0.00	0.88	0.88	0.88	0.88	0.00	0.00	0.00	0.75	0.75	0.75	0.75
β-catenin	0.00	0.00	0.00	0.01	1.00	0.01	1.00	0.00	0.00	0.00	0.13	0.89	0.13	0.90
HIF	0.00	0.00	0.00	0.96	0.96	0.95	0.95	0.01	0.01	0.01	0.91	0.91	0.90	0.90
NFκB	0.00	0.00	0.00	0.30	0.30	0.30	0.30	0.00	0.00	0.00	0.36	0.36	0.36	0.36
iκB	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.04	0.04	0.04
TNF-α	0.00	0.00	0.00	0.45	0.45	0.45	0.45	0.00	0.00	0.00	0.41	0.41	0.41	0.41
IL10	0.00	0.00	0.00	0.42	0.42	0.42	0.42	0.00	0.00	0.00	0.37	0.37	0.37	0.37
IL1	0.00	0.00	0.00	0.42	0.42	0.42	0.42	0.00	0.00	0.00	0.35	0.35	0.35	0.35
IL8	0.00	0.00	0.00	0.45	0.45	0.45	0.45	0.00	0.00	0.00	0.51	0.51	0.51	0.51
FasL	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.04	0.04	0.04	0.04
COX2	0.00	0.00	0.00	0.46	0.46	0.46	0.46	0.00	0.00	0.00	0.51	0.51	0.51	0.51
TGF-β	0.00	0.00	0.00	0.98	0.98	0.98	0.98	0.00	0.00	0.00	0.64	0.64	0.64	0.64
IFNγ	0.00	0.00	0.00	0.20	0.20	0.20	0.20	0.00	0.00	0.00	0.20	0.20	0.20	0.20
STAT3	0.00	0.00	0.00	0.18	0.18	0.18	0.18	0.00	0.00	0.00	0.26	0.27	0.26	0.27
GSK3β	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.99	0.99	0.99	0.09	0.09	0.09	0.09
Gastrin	0.00	0.00	0.00	0.00	1.00	0.00	1.00	0.00	0.00	0.00	0.02	0.88	0.02	0.88
Sox2	0.88	0.00	0.00	0.95	0.04	0.95	0.04	0.87	0.00	0.00	0.86	0.20	0.86	0.19
Cdx2	0.00	0.00	0.99	0.00	1.00	0.00	1.00	0.00	0.00	0.87	0.00	0.87	0.00	0.88
Shh	0.01	0.00	0.00	0.95	0.00	0.95	0.00	0.08	0.00	0.00	0.86	0.01	0.86	0.01

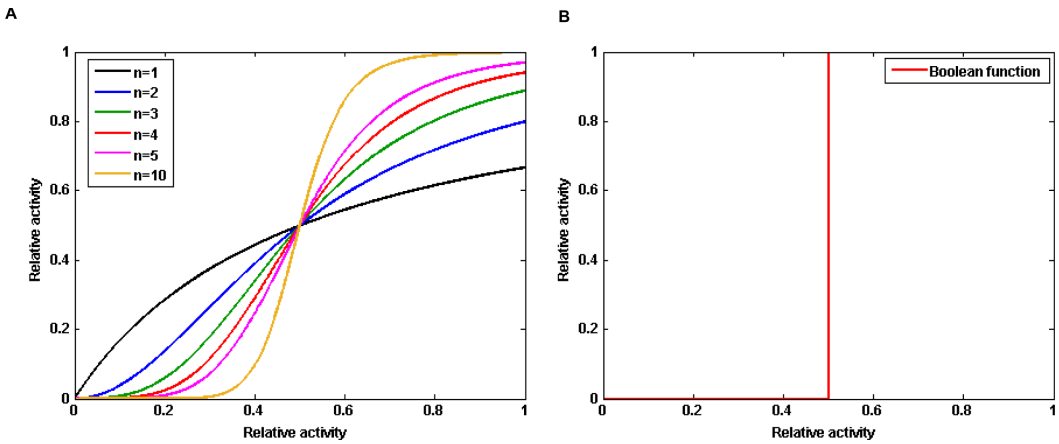
Supplementary Table S17: Invariant saddle points of working endogenous network under random parameter $n_i (3 \leq n_i \leq 10; i = 1, 2, ..., 215)$ and $a_i = 2^{n_i}$

Random Parameter n_i=[1,10], $a=2^{ni}$, i=1,2,…,215.													
Components	S_1	S_2	S_3	S_4	S_5	S_6	S_7	S_8	S_9	S_{10}	S_{11}	S_{12}	S_{13}
Neighbor stable states	A_1,R_1	R_1,P_1	R_1,R_2	R_2,P_2	P_1,P_2	R_1,R_2,P_1,P_2	A_1,A_2	A_1,A_2	A_2,A_3	A_2,A_3	A_1,D	A_2,D	A_3,D
Rb	1.00	0.17	0.83	0.02	0.01	0.16	1.00	0.68	1.00	1.00	0.68	0.68	1.00
Cyclin D/Cdk4,6	0.03	0.03	0.40	1.00	0.52	0.52	0.00	0.00	0.00	(0.00)	0.00	0.00	0.00
Cyclin E/Cdk2	0.00	0.62	0.00	0.50	1.00	0.60	(0.00)	0.00	0.00	0.00	0.00	(0.00)	(0.00)
Myc	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
E2F	0.00	0.53	0.00	0.50	0.98	0.52	0.00	(0.00)	0.00	(0.00)	0.00	(0.00)	(0.00)
p21	0.38	0.07	0.07	0.07	0.07	0.07	(0.00)	0.24	0.57	0.50	0.24	0.24	1.00
p27	0.05	0.00	0.00	0.00	0.00	0.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
p53	0.10	0.03	0.01	0.02	0.04	0.03	0.00	0.44	0.44	(0.00)	0.44	0.44	0.44
Caspase 3,7	0.12	0.05	0.10	0.10	0.05	0.05	0.00	0.43	0.14	0.00	0.43	0.43	0.01
Cytochrome *c*	0.08	0.01	0.01	0.01	0.01	0.01	(0.00)	0.48	0.48	0.00	0.48	0.48	0.48
Caspase 8,10	0.41	0.49	0.84	0.84	0.49	0.49	0.00	0.20	0.20	(0.00)	0.20	0.20	0.20
XIAP	0.50	0.92	0.92	0.92	0.92	0.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bcl-2	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bcl-xL	0.66	0.98	0.98	0.98	0.98	0.98	(0.00)	(0.00)	(0.00)	(0.00)	0.00	(0.00)	(0.00)
Bid	0.39	0.49	0.79	0.79	0.49	0.49	0.00	0.11	0.11	0.00	0.11	0.11	0.11
Bad	0.00	0.00	0.00	0.00	0.00	0.00	(0.00)	0.35	0.35	(0.00)	0.35	0.35	0.35
Bax	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.43	0.00	0.43	0.43	0.43
Ras	0.95	0.98	0.98	0.98	0.98	0.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Akt	0.50	1.00	1.00	1.00	1.00	1.00	0.04	0.03	0.04	0.04	0.03	0.03	0.04
PTEN	0.49	0.00	0.00	0.00	0.00	0.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
ERK	0.45	0.45	0.45	0.45	0.45	0.45	0.00	0.00	0.00	(0.00)	0.00	0.00	0.00
JNK/p38	0.40	0.45	0.45	0.45	0.45	0.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MKP	0.44	0.51	0.51	0.51	0.51	0.51	(0.00)	(0.00)	0.00	0.00	(0.00)	0.00	0.00
VEGF/VEGFR	0.87	1.00	1.00	1.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
EGF/EGFR	0.51	0.98	0.98	0.98	0.98	0.98	(0.00)	(0.00)	(0.00)	0.00	0.00	0.00	0.00
IGF/IGFR	0.49	0.98	0.98	0.98	0.98	0.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00
HGF/c-Met	0.61	0.95	0.95	0.97	0.95	0.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Integrin/FAK	0.46	1.00	1.00	1.00	1.00	1.00	0.00	(0.00)	(0.00)	(0.00)	0.00	(0.00)	(0.00)
E-cadherin	0.07	0.01	0.01	0.01	0.01	0.01	1.00	0.72	1.00	1.00	0.72	0.72	1.00
Zeb1/2	0.66	0.88	0.88	0.88	0.88	0.88	0.00	(0.00)	0.00	(0.00)	(0.00)	(0.00)	(0.00)
β-catenin	0.01	0.01	0.58	1.00	0.62	0.62	0.00	0.00	(0.00)	0.00	0.00	0.00	0.00
HIF	0.50	0.96	0.96	0.96	0.95	0.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NFκB	0.14	0.30	0.30	0.30	0.30	0.30	0.00	(0.00)	0.00	(0.00)	0.00	0.00	(0.00)
iκB	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
TNF-α	0.44	0.45	0.70	0.70	0.45	0.45	(0.00)	0.00	0.00	0.00	(0.00)	0.00	0.00
IL10	0.40	0.42	0.38	0.38	0.42	0.42	0.00	0.26	0.26	(0.00)	0.26	0.26	0.26
IL1	0.30	0.42	0.42	0.42	0.42	0.42	0.00	(0.00)	0.00	(0.00)	(0.00)	0.00	(0.00)
IL8	0.30	0.45	0.45	0.45	0.45	0.45	(0.00)	0.00	0.00	0.00	(0.00)	0.00	0.00
FasL	0.00	0.01	0.02	0.02	0.01	0.01	(0.00)	0.38	0.38	(0.00)	0.38	0.38	0.38
COX2	0.27	0.46	0.46	0.46	0.46	0.46	(0.00)	(0.00)	0.00	0.00	(0.00)	0.00	(0.00)
TGF-β	0.61	0.98	0.98	0.98	0.98	0.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IFNγ	0.04	0.20	0.51	0.51	0.20	0.20	(0.00)	(0.00)	(0.00)	(0.00)	0.00	(0.00)	0.00
STAT3	0.34	0.18	0.18	0.18	0.18	0.18	0.00	0.10	0.10	0.00	0.10	0.10	0.10
GSK3β	0.50	0.00	0.00	0.00	0.00	0.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Gastrin	0.00	0.00	0.88	1.00	0.87	0.87	0.00	(0.00)	0.00	0.00	(0.00)	0.00	0.00
Sox2	0.90	0.95	0.48	0.02	0.47	0.47	0.50	0.50	0.01	0.00	0.88	0.01	0.01
Cdx2	0.00	0.00	0.41	1.00	0.52	0.52	0.00	(0.00)	0.50	0.50	(0.00)	0.00	0.99
Shh	0.48	0.95	0.59	0.00	0.18	0.18	0.01	0.01	0.00	0.00	0.01	0.00	(0.00)

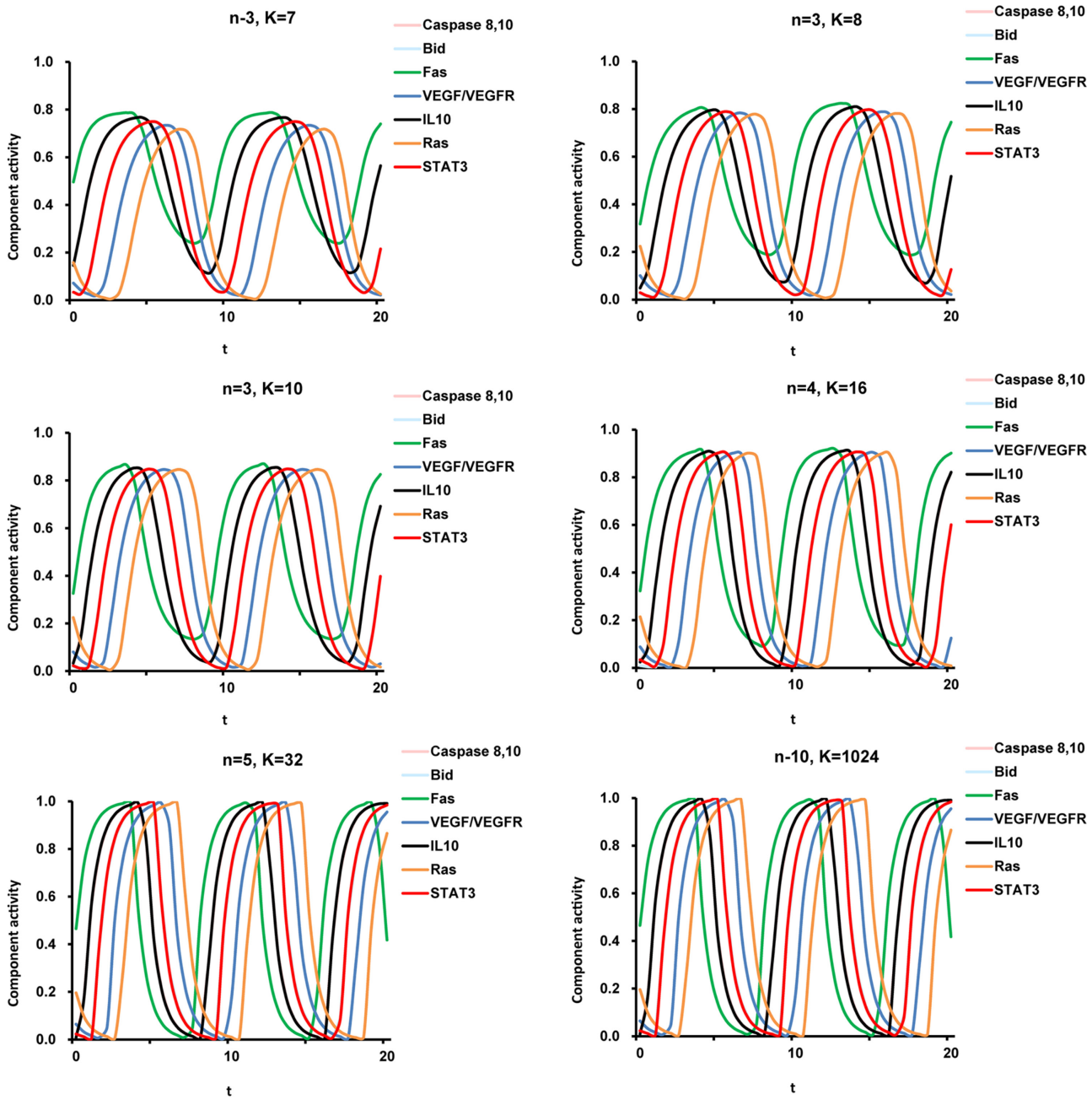
Supplementary Table S18: Consistence between attractors of ordinary diferential equations (ODE) model and Boolean network. Note that there are cyclic attractors in ODE model and Boolean network, the listed are average activity profiles

	Attractors of ODE model							Attractors of Boolean Network						
Endogenous factors	A_1	A_2	A_3	D	R_1	P_1	P_2	A_1	A_2	A_3	D	R_1	P_1	P_2
Rb	1.00	1.00	1.00	0.98	0.95	0.14	0.08	1.00	1.00	1.00	0.67	0.25	0.00	0.00
Cyclin D/Cdk4,6	0.00	0.00	0.00	0.00	0.12	0.12	0.83	0.00	0.00	0.00	0.00	0.50	0.50	0.75
Cyclin E/Cdk2	0.00	0.00	0.00	0.00	0.15	0.84	0.86	0.00	0.00	0.00	0.00	0.25	1.00	1.00
Myc	0.01	0.01	0.00	0.00	0.26	0.26	0.26	0.00	0.00	0.00	0.00	0.25	0.25	0.25
E2F	0.00	0.00	0.00	0.05	0.02	0.82	0.86	0.00	0.00	0.00	0.00	0.00	1.00	1.00
p21	0.00	0.00	0.86	0.87	0.09	0.09	0.09	0.00	0.00	1.00	0.67	0.00	0.00	0.00
p27	0.96	0.95	0.95	0.96	0.08	0.05	0.04	1.00	1.00	1.00	1.00	0.00	0.00	0.00
p53	0.00	0.00	0.00	0.88	0.04	0.08	0.08	0.00	0.00	0.00	0.67	0.00	0.00	0.00
Caspase 3,7	0.00	0.00	0.00	0.12	0.07	0.07	0.07	0.00	0.00	0.00	0.33	0.00	0.00	0.00
Cytochrome c	0.00	0.00	0.00	0.93	0.04	0.05	0.05	0.00	0.00	0.00	0.67	0.00	0.00	0.00
Caspase 8,10	0.00	0.00	0.00	0.42	0.53	0.53	0.53	0.00	0.00	0.00	0.33	0.75	0.75	0.75
XIAP	0.01	0.01	0.01	0.00	0.91	0.91	0.91	0.00	0.00	0.00	0.00	1.00	1.00	1.00
Bcl-2	0.01	0.00	0.00	0.03	0.25	0.25	0.24	0.00	0.00	0.00	0.00	0.50	0.50	0.50
Bcl-xL	0.00	0.00	0.00	0.00	0.79	0.79	0.79	0.00	0.00	0.00	0.00	0.75	0.75	0.75
Bid	0.00	0.00	0.00	0.43	0.60	0.59	0.60	0.00	0.00	0.00	0.33	0.75	0.75	0.75
Bad	0.00	0.00	0.00	0.87	0.00	0.00	0.00	0.00	0.00	0.00	0.67	0.00	0.00	0.00
Bax	0.00	0.00	0.00	0.87	0.02	0.03	0.03	0.00	0.00	0.00	0.67	0.00	0.00	0.00
Ras	0.00	0.00	0.00	0.48	0.97	0.97	0.97	0.00	0.00	0.00	0.33	1.00	1.00	1.00
Akt	0.08	0.08	0.08	0.08	0.97	0.97	0.98	0.00	0.00	0.00	0.00	1.00	1.00	1.00
PTEN	0.99	0.99	0.99	1.00	0.09	0.09	0.06	1.00	1.00	1.00	1.00	0.00	0.00	0.00
ERK	0.00	0.00	0.00	0.06	0.38	0.38	0.38	0.00	0.00	0.00	0.00	0.50	0.50	0.50
JNK/p38	0.00	0.00	0.00	0.04	0.38	0.38	0.39	0.00	0.00	0.00	0.00	0.50	0.50	0.50
MKP	0.00	0.00	0.00	0.00	0.53	0.53	0.53	0.00	0.00	0.00	0.00	0.50	0.50	0.50
VEGF/VEGFR	0.01	0.01	0.01	0.45	0.97	0.97	0.97	0.00	0.00	0.00	0.33	1.00	1.00	1.00
EGF/EGFR	0.00	0.00	0.00	0.00	0.90	0.90	0.91	0.00	0.00	0.00	0.00	1.00	1.00	1.00
IGF/IGFR	0.00	0.00	0.00	0.00	0.88	0.88	0.88	0.00	0.00	0.00	0.00	1.00	1.00	1.00
HGF/c-Met	0.00	0.00	0.00	0.00	0.89	0.89	0.94	0.00	0.00	0.00	0.00	1.00	1.00	1.00
Integrin/FAK	0.00	0.00	0.00	0.00	0.93	0.93	0.94	0.00	0.00	0.00	0.00	1.00	1.00	1.00
E-cadherin	1.00	1.00	1.00	0.98	0.05	0.05	0.05	1.00	1.00	1.00	0.67	0.00	0.00	0.00
Zeb1/2	0.00	0.00	0.00	0.00	0.75	0.75	0.75	0.00	0.00	0.00	0.00	0.75	0.75	0.75
β-catenin	0.00	0.00	0.00	0.00	0.13	0.13	0.90	0.00	0.00	0.00	0.00	0.50	0.50	0.75
HIF	0.01	0.01	0.01	0.00	0.91	0.90	0.90	0.00	0.00	0.00	0.00	1.00	1.00	1.00
NFκB	0.00	0.00	0.00	0.00	0.36	0.36	0.36	0.00	0.00	0.00	0.00	0.50	0.50	0.50
iκB	0.00	0.00	0.00	0.00	0.04	0.04	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00
TNF-α	0.00	0.00	0.00	0.00	0.41	0.41	0.41	0.00	0.00	0.00	0.00	0.50	0.50	0.50
IL10	0.00	0.00	0.00	0.42	0.37	0.37	0.37	0.00	0.00	0.00	0.33	0.25	0.25	0.25
IL1	0.00	0.00	0.00	0.00	0.35	0.35	0.35	0.00	0.00	0.00	0.00	0.50	0.50	0.50
IL8	0.00	0.00	0.00	0.00	0.51	0.51	0.51	0.00	0.00	0.00	0.00	0.75	0.75	0.75
Fas	0.00	0.00	0.00	0.42	0.04	0.04	0.04	0.00	0.00	0.00	0.33	0.00	0.00	0.00
COX2	0.00	0.00	0.00	0.00	0.51	0.51	0.51	0.00	0.00	0.00	0.00	0.75	0.75	0.75
TGF-β	0.00	0.00	0.00	0.00	0.64	0.64	0.64	0.00	0.00	0.00	0.00	0.50	0.50	0.50
IFN-γ	0.00	0.00	0.00	0.00	0.20	0.20	0.20	0.00	0.00	0.00	0.00	0.50	0.50	0.50
STAT3	0.00	0.00	0.00	0.43	0.26	0.26	0.27	0.00	0.00	0.00	0.33	0.50	0.50	0.50
GSK3β	0.99	0.99	0.99	0.99	0.09	0.09	0.09	1.00	1.00	1.00	1.00	0.00	0.00	0.00
Gastrin	0.00	0.00	0.00	0.00	0.02	0.02	0.88	0.00	0.00	0.00	0.00	0.50	0.50	0.75
Sox2	0.87	0.00	0.00	0.89	0.86	0.86	0.19	1.00	0.00	0.00	1.00	0.50	0.50	0.25
Cdx2	0.00	0.00	0.87	0.00	0.00	0.00	0.88	0.00	0.00	1.00	0.00	0.00	0.00	0.50
Shh	0.08	0.00	0.00	0.08	0.86	0.86	0.01	0.00	0.00	0.00	0.00	0.50	0.50	0.00

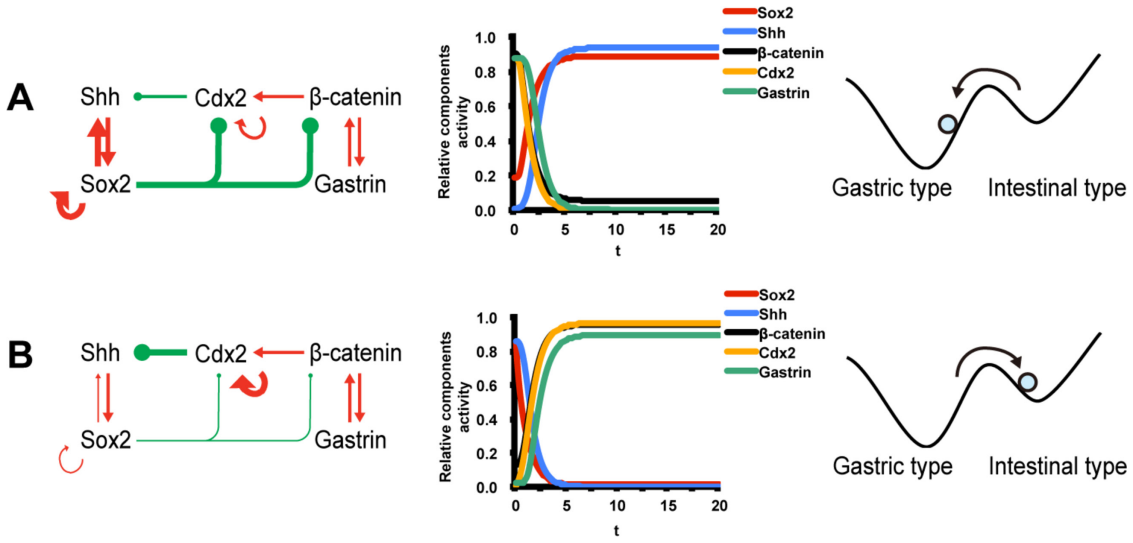
Supplementary Table S19: Comparing model predictions and relative expression change of downstream nodes of signaling pathways. The gene expression of downstream nodes of some signaling pathways, including Ras/MAPK, VEGF, NF-κB and Wnt/β-catenin signaling were checked in high-throughput data. The comparison indicated that 67% (GSE 19826) and 66.7% (GSE 22183) of the relative gene expression changes of downstream nodes predicted by the modeling results were consistent with high-throughput data.



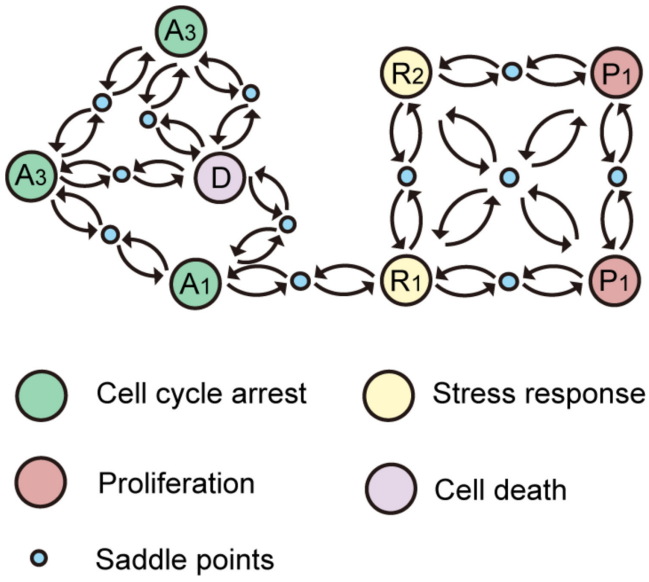
Supplementary Figure S1: Hill functions and Boolean functions. Hill functions with Hill coefficients n = 1, 2, 3, 4, 5, 10 and $a = 2^n$ as continuous relaxation of a Boolean step function. **A.** Hill functions; **B.** Boolean functions.



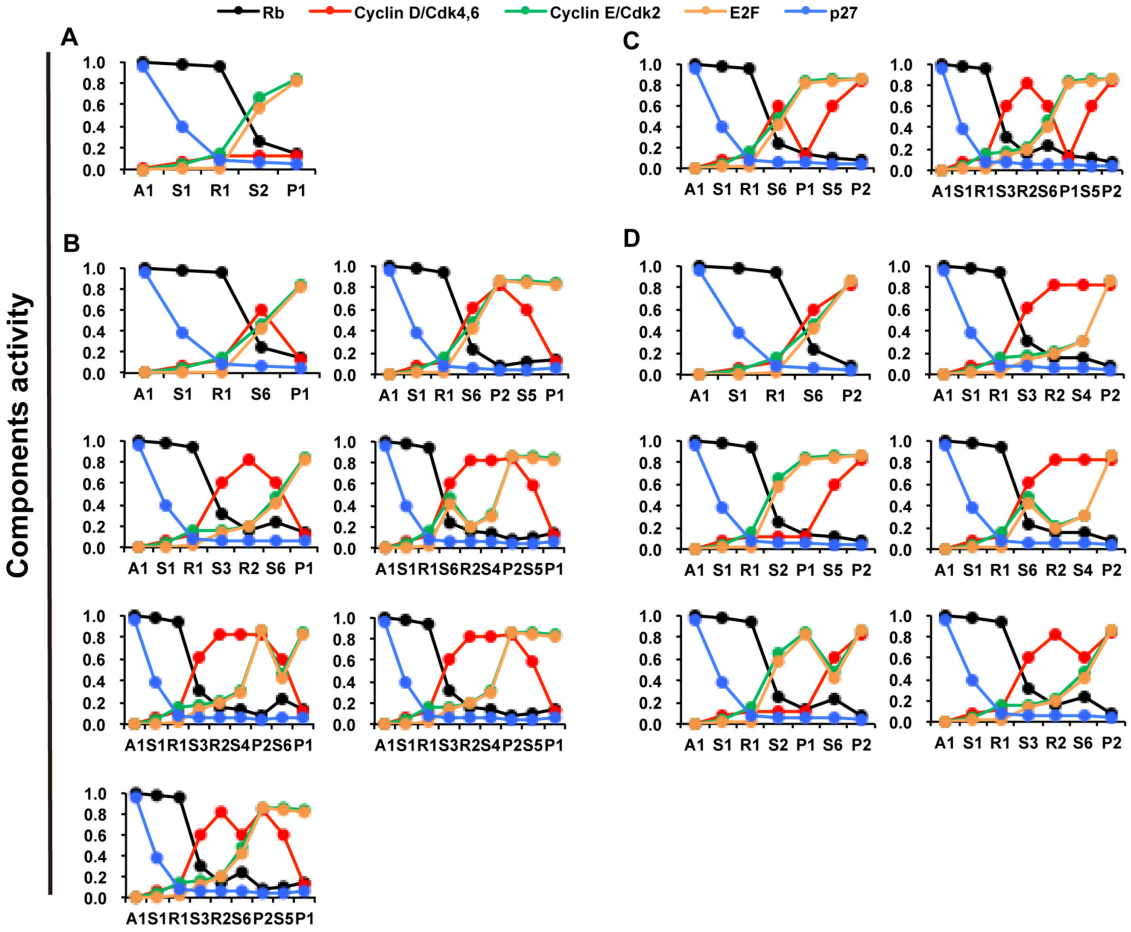
Supplementary Figure S2: Calculated dynamical trajectories of cell death attractor under scanning parameters. Dynamical trajectories of Caspase 8/10, Bid, Fas, VEGF/VEGFR, IL10, Ras and STAT3.



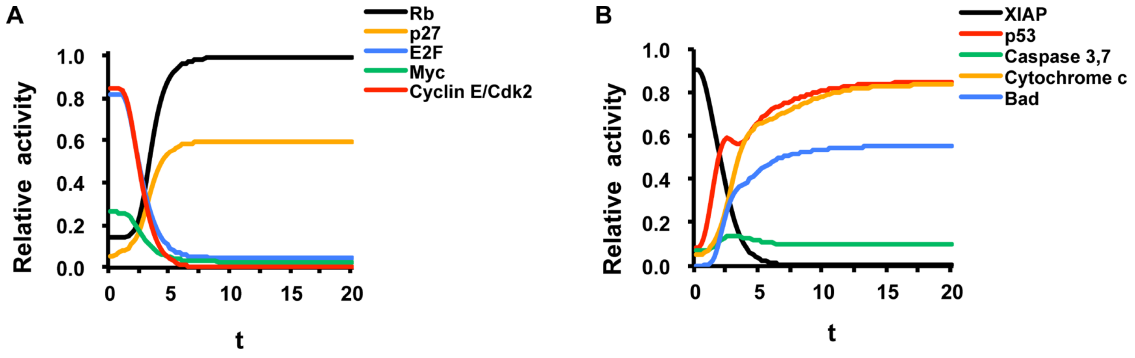
Supplementary Figure S3: Transition between gastric- and intestinal-type attractors. The working model indicated that intestinal-type attractor can be induced to gastric-type attractor by consistently activating Sox2 (Supplementary Figure S2A), whereas gastric-type attractor can be induced to intestinal-type attractor by activating Cdx2 and inhibiting Sox2 simultaneously (Supplementary Figure S2B).



Supplementary Figure S4: Schematic illustration of the functional landscape for the core endogenous molecular network of gastric epithelium. Large circles represent attractors indicating 8 cellular phenotypes. Blue circles represent saddle points, which are unstable equilibrium states. Arrows denote that a transition can occur between two attractors. A_1, A_2 and A_3, cell cycle arrest; D, cell death; R_1 and R_2, stress response; P_1 and P_2, proliferation.



Supplementary Figure S5: Dynamics of cell cycle components in the routes of GC progression. A–D. shows activity dynamics of cell cycle components in 16 possible inherent evolutional routes from normal gastric epithelial attractor A_1 to GC attractors P_1 and P_2. The dynamic process of certain critical regulators exhibit 4 major patterns of GC progression: **A.**-(.A_1, A_2 and A_3, cell cycle arrest; D, cell death; R_1 and R_2, stress response; P_1 and P_2, proliferation; S1–S14, saddle points.



Supplementary Figure S6: Dynamics of cell cycle and apoptosis components activities under consistently inhibiting PI3K/Akt activity. A. When PI3K/Akt activity was manually inhibited in GC attractor, the activities of cell cycle components E2F, Myc and CyclinE/Cdk2 were inhibited, while the activities of cell cycle arrest related components Rb and p27 were activated. GC attractor transformed to cell cycle arrest like attractor by consistently inhibiting PI3K/Akt activity. **B.** When PI3K/Akt activity was manually inhibited in GC attractor, the activities of anti-apoptotic components XIAP was inhibited, while the activities of pro-apoptotic related components p53, Cytochrome *c* and Bad were activated. GC attractor transformed to apoptosis like attractor by consistently Inhibiting PI3K/Akt activity.